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OM nucleic - nucleic search, using sw model

Run on: October 3, 2003, 15:11:02 : Search time 151 Seconds

(without alignments)

6313.825 Million cell updates/sec

Title: US-09-965-825-1

Perfect score: 2160

Sequence: 1 ttagagcgagcttctgtgaggg.....ggtgccatgagatgcctt 2160

Scoring table:

IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/prodata/1/lna/5A.COMB.seq:*
2: /cgn2_6/prodata/1/lna/5B.COMB.seq:*
3: /cgn2_6/prodata/1/lna/6A.COMB.seq:*
4: /cgn2_6/prodata/1/lna/6B.COMB.seq:*
5: /cgn2_6/prodata/1/lna/PCFUS.COMB.seq:*
6: /cgn2_6/prodata/1/lna/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	269.4	12.5	1737	4	US-09-252-991A-7335
2	164.2	7.6	1083	4	US-09-252-991A-7413
3	164.2	7.6	1113	4	US-09-252-991A-7281
4	129.6	6.0	798	4	US-09-252-991A-7166
5	110.2	5.1	1746	4	US-09-107-532A-3181
6	101.6	4.7	1761	4	US-09-134-001C-1619
7	100.4	4.6	2577	4	US-09-252-991A-8458
8	100.4	4.6	2754	4	US-09-252-991A-8530
9	87.2	4.0	260	3	US-08-735-543-24
10	87.2	4.0	260	3	US-09-449-083-24
11	81.2	3.8	1443	4	US-09-252-991A-8318
12	60.8	2.8	2841	2	US-08-452-075-1
13	60.8	2.8	2841	3	US-09-231-061-1
14	60.8	2.8	2841	4	US-09-011-762-5
15	59.8	2.8	25002	4	US-08-961-527-48
16	58	2.7	4403765	3	US-09-103-840A-2
17	58	2.7	4411529	3	US-09-103-840A-1
18	55.8	2.6	1830121	4	US-09-557-884-1
19	55.8	2.6	1830121	4	US-09-643-990A-1
20	53.4	2.5	3390	3	US-09-550-338-1
21	50.6	2.3	6211	4	US-08-961-527-8
22	49.4	2.3	2365	4	US-08-363-208-1
23	49.4	2.3	2365	3	US-09-137-478-1
24	48.6	2.2	1800	4	US-09-252-991A-3891
25	48.6	2.2	1824	4	US-09-252-991A-4025
26	48.6	2.2	1875	4	US-09-252-991A-3919
27	48.4	2.2	1664976	4	US-08-916-421B-1

ALIGNMENTS

28	48.2	2.2	1969	1	US-07-737-851-1	Sequence 1, Appl1
29	48.2	2.2	1969	1	US-07-737-851-2	Sequence 2, Appl1
30	48.2	2.2	1969	1	US-07-737-851-3	Sequence 3, Appl1
31	48.2	2.2	1969	1	US-07-894-062-1	Sequence 1, Appl1
32	48.2	2.2	1969	1	US-07-894-062-2	Sequence 2, Appl1
33	48.2	2.2	1969	1	US-07-894-062-3	Sequence 3, Appl1
34	48.2	2.2	1969	4	US-09-096-562-1	Sequence 1, Appl1
35	48.2	2.2	1969	4	US-09-096-562-2	Sequence 2, Appl1
36	48.2	2.2	1969	4	US-09-096-562-3	Sequence 3, Appl1
37	47.6	2.2	2156	1	US-08-321-356-1	Sequence 1, Appl1
38	47.6	2.2	2156	1	US-08-321-356-2	Sequence 2, Appl1
39	47.2	2.2	3390	3	US-09-550-338-1	Sequence 1, Appl1
40	47	2.2	1731	4	US-09-328-352-3942	Sequence 3, Appl1
41	47	2.2	1882	1	US-08-458-120-1	Sequence 1, Appl1
42	47	2.2	1882	2	US-08-867-970-1	Sequence 1, Appl1
43	47	2.2	1882	3	US-09-326-217-1	Sequence 1, Appl1
44	47	2.2	1882	4	US-09-732-020-1	Sequence 1, Appl1
45	46.4	2.1	1735	4	US-09-134-001C-1047	Sequence 1047, Ap

RESULT 1

US-09-252-991A-7335
Sequence 7335, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252.991A

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/000 788

PRIOR FILING DATE: 1998-07-22

PRIOR APPLICATION NUMBER: 90

PRIOR FILING DATE: 1998-07-22

PRIOR APPLICATION NUMBER: 90

PRIOR FILING DATE: 1998-07-22

PRIOR APPLICATION NUMBER: 90

PRIOR FILING DATE: 1998-07-22

PRIOR APPLICATION NUMBER: 90

PRIOR FILING DATE: 1998-07-22

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PRIOR APPLICATION NUMBER: 90

PRIOR FILING DATE: 1998-07-22

PRIOR APPLICATION NUMBER: 90

PRIOR FILING DATE: 1998-07-22

PRIOR APPLICATION NUMBER: 90

PRIOR FILING DATE: 1998-07-22

PRIOR APPLICATION NUMBER: 90

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Db      1461 CTTGCTCAACCCGGAGCTTGCCTCGTCCGCGGAAGTATCGGCTTCCACGAGCAAGT 1520
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      1838 CACCGATCCGAGAAAGTTGCGCAGCAGCTAGCTAGAGCATTTGGCATATCTCGACCTGT 1897
              || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1521 GACCGCGCTCCGAGAGAGTCCGAGACGGCGGCTGCAAGAGATTCTCGCCACGCGGCTCGGC 1580
              || | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      1898 ACATGATGATATGCTGCACGATCCTAATGCGCTGATCCACCAACCATCATGCTGGGA 1957
              || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1581 GCTGCTGAGAGTGCATACCAACCTCGCGGAGCTGTATGCTGCCGAGAAAGATCGAGTTCCG 1640
              || | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      1958 ACAAGTCT 1964
              || | | | |
Db      1641 CCAAGTCT 1647

RESULT 2
US-09-252-991A-7413
; Sequence 7413, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 35142
; SEQ ID NO 7413
; LENGTH: 1083
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7413

Query Match      7.6%; Score 164.2; DB 4; Length 1083;
Best Local Similarity 50.9%; Pred. No. 5,2e-41;
Matches 469; Conservative 0; Mismatches 443; Indels 9; Gaps 3;

Oy      341 CGCGAACAAATTAATGACACTTGGAAAGCTCAAGGTGTGAAGCATTTATGGTTGGT 400
              || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      42  CGCGAGATCGTCTGGAAACCTTGAAGCCGCGCGCTCCGCATTGCTATGGCATCTGT 101
              || | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      401 GGGTGAGACGCTTATCCGATCGTGAATGCTGTCGCGCAATCAGATATTGAGTGGTGC 460
              || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      102 CGGGGACACCTTCACCATGTCACCGAGCCATCATTCAGCGCAAGATCCAGTGGGTCCA 161
              || | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      461 CGTTGGAATGAGAAAGCGGCGGCTTTGCAAGCCGCGGTGCGAATCGTTGATCAGTGGGA 520
              || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      162 CGTCGCGCAGCAAAACGCGGCGCTTCGCGCGCGGCGCGCAAGTCTCAATCACGGAACG 221
              || | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      521 GCTGCGAGTATGTCCTCTTCTTGTGTCCTCGAAACACACACACCATGATTGAGGCTCTTA 580
              || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      222 CCGTACGCGCTCGCGCGGCTCTCTCGGACCGCGGAGCCTGTGCACTTCAATCAAGGCGCTGA 281
              || | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      581 TGATTGCAATGGAATGTGCGAAGGTGTGGCCATCGTACGATATTCGAGTCCCA 640
              || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      282 CGAAGGCCAGGCAACCGCGCGCGATGATGCTGATGCGCAGCATCGTTACCCGCA 341
              || | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      641 GATTGCTTCAAGCTTTCACGAAAGCAATCCGCGAATTTTGTTAAAGAAATGCTCTGG 700
              || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      342 ACTGGGATGAGTTTCCCAAGAGGTGCAATTAAGCGGCTTACGCCAGCTGCTGAGT 401
              || | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      701 TTACTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 760
              || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      402 GTTCTGGAGAGAGGTGACAGCCCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 461
              || | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy      761 GTCCACCATGCGCGGTAAAGTGTGTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGA 820
              || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      462 GGGCGGCGCTCAACCGCGCGCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 517
              || | | | | | | | | | | | | | | | | | | | | | | | | | |

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Query Match	7.6%	Score 164.2	DB 4	Length 1113
Best Local Similarity	50.9%	Pred. No. 5.2e-41		
Matches 465	Conservative 0	Mismatches 443	Indels 9	Gaps 3
QY	341	CGCAGAACAAATTAATTGACACTTTGGAAGCTCAAGTGTGAAGCAATTAATGGTTGGT	400	
Db	1060	CGCGAGATCGTGTGGAAACCCCTGGAAGCCGGGGGTCCGCCATTGCTATGGCATCGT	1001	
QY	401	GGGTGACAGCCTTAATCCGATCGTGGATGCTGTCCGCATACATATATGAGGGGTGCA	460	
Db	1000	CGCGCACACCCCTCAACCATGTCAACCGACGCCATCCATCGCAGCCAGATCCAGTGGTCCA	941	
QY	461	CGTTGCAATGAGAGAACCGCGGGGTTTGACGCCGGGCGGAATCGTTGATCACTGGGGA	520	
Db	940	CGTCCGCCACGAAGAAAGCGCGGCTCTCCGCCGGGGCGGAGTCTCACTACACGGGACG	881	
QY	521	GCTGGCAGTATGCTGCTCTTGTGTGGTCCGGAACACACACACACTGATTCAGGGTCTTTA	580	

RESULT 4
 US-09-252-991A-7166/C
 Sequence 7166, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 10/7196,136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 7166
 LENGTH: 798
 TYPE: DNA
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-7166

Query Match 6.0%; Score 129.6; DB 4; Length 798;
 Best Local Similarity 52.6%; Pred. No. 2.8e-30;
 Matches 307; Conservative 0; Mismatches 274; Indels 3; Gaps 1;

1381 ACCTCGAGAGCATGTGCTTATTCACCCCTGAAATACGTTGCTCTATTTTGAACGAGCTGG 1440
 644 AAGCCGCGCAAGGGCGACCTGATCCATCCGAGACCTGGACCCCTGCTGACACGACGAG 585
 1441 CGGATGAGATGCGGTGTACTGTGATGACGCAATGTCATGTTGTGTGATGCGAGGT 1500
 584 CCAAGGAGAGAGCCCTGTTTACACCGGAGCGGCGCTGCGGATGTTGCTGTGCTGCTG 525
 1501 ACATCGAGATCCGAGAGAGCGCGGACTTTGTGGTTTATTCGCCACGAGCGACGATGG 1560
 524 ACATCCACA--GCAAGCGCAAGCGCGGACCCCTCAACACCTGTGTCTCAGCGACCATG 468
 1561 CTATGCTGCTCATGATGATGTTGGCAAGTGTGTATGCAACCGCGAGGTATGG 1620
 467 CCAAGCGCATGCCCCAGCGCTGAGGCTGAGAGAGGCTTACCCGAGCGGAGGTGATCT 408
 1621 CGATGCTGCGCATGATGTTGTTGGGATGCTGCTGCTGAGTGAAGTCTTGACCGTTAAGCTGG 1680
 407 CGATCTCCGCGAGAGCGGCGCTGAGCATGCTGCTGCTGCGGACCTGTGAGCGGACCATG 348
 1681 ACCAGCTCGCGTGAAGGCTGTGTTTAAACAAGTCTTGGCGGATGCGGATGAGTTGG 1740
 347 AAAAAGTCCGATCAAGTGTGTGTGTGTAACATGCTGCTGCTGTAAGTCTGCTGAGCTGG 288
 1741 AGATGCTGTGAGAGGAGACACCAATTTGTACTGACATGCAATGAGAGATGAAATTTGCGAG 1800
 287 AACAGAGTCTGAGAGGCGCTGTGAGACAGTACACCGACTGTCTCAACCCGAGTGTGCGCC 228
 1801 AGATGCGCGGCTGCGGCTATCAATCGGTACCGCATCCGATCCGAGAAAGTTGCGG 1860
 227 GTCTGCGGAGAGTGTGCTTCCACGAGCGAAGGAGCGGCTCCGAGAGCTCGAGA 168
 1861 AGCAGTAGCTGAGAGGATTTGCAATTCCTGACCTGATGATGATGATGATGATGATGATG 1920
 167 CGGCGGTGAGAGATGCTTCCGCGGAGCGGCTGCGGCGTGTGAGAGTGTCAATACCAAC 108
 1921 CTATGCGGCTGTGATGCTCCACCAACCATTCACGTTGGAGAGGTC 1964
 107 CTGCGGAGCTGTGTATGCGCGGAGATGAGTTGGCGCAGGTC 64

Db

RESULT 5
 US-09-107-532A-3181
 ; Sequence 3181, Application US/09107532A
 ; Patent No. 6583275
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn A Doucette-Stamm and David Bush
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 ; NUMBER OF SEQUENCES: 7310
 ; CORRESPONDENCE ADDRESS: 7310
 ; ADDRESSSEE: GENOME THERAPEUTICS CORPORATION
 ; STREET: 100 Beaver Street
 ; CITY: Waltham
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02354
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: CD-ROM ISO9660
 ; COMPUTER: PC
 ; OPERATING SYSTEM: <Unknown>
 ; SOFTWARE: ASCII
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 30-Jun-1998
 ; APPLICATION NUMBER: US/09/107,532A
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/085,598
 ; FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Arinaello, Pamela Denke
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 3181:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1746 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (b) LOCATION 1...1746
 SEQUENCE DESCRIPTION: SEQ ID NO: 3181:
 US-09-107-532A-3181

Query Match 5.1%; Score 110.2; DB 4; Length 1746;
 Best Local Similarity 44.2%; Pred. No. 4.9e-24;
 Matches 653; Conservative 0; Mismatches 803; Indels 21; Gaps 4;

439 AATGATATTTAGTGGGTGACGATTCGAAATAGAGAAAGCGGCGTTGCGAGCGGTG 498
 137 AATGCAATATCAATCATTCATTCAGATTCGATGAAAGAGTGGCGACACGCGCGT 196
 499 CGGATGCTGTATCACTGGGAGCTGGCGAGTATGTGCTGCTTGTGTGCTCGAAGCA 558
 197 CAGATCAAAATTAACGGGAGAAAGTGGCGTGTCTCGGCTCTGAGAGCTGTGCGA 256
 559 CACACCTGATGAGGCTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 618
 257 CACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 316
 619 CTAGCCATATTCGAGTGGCCAGATTTGTCAGCTTCTTCAGAGAAACGATCCGAGGA 678
 317 TAGGACAAAGTGTCTTACATCATCATGATATGATGATGATGATGATGATGATGATGAT 376
 679 TTTGTTAAGGATGCTGCTGTTACTGCGAGATGATGATGATGATGATGATGATGATGAT 738
 377 CTATTTTCCAGATGTTTACGCTATACAAATCGTACATGATGACACACCAAAATCTTCCG 436
 739 GATTTTGCATCAGGATTCAGTCCACCATGAGCGGTAAGGTGTGCGTGTAGTGA 798
 437 ATGTAGTATGATGAGCATTAAGCGCGCTATGAGATTAAGCGGTGCTATCGTACGA 496
 799 TTCTGTGATATGCTAAGAGAGAGCGAGGTGAGGTCTTATTCATTCATTCATTT 858
 497 TCCCTTTGATGCTGTTTGAAGAAATGAGCAACACCTTTCCCA--CGGTCCACA 553
 859 CTTCTGCACTCTCTGTGCTTCCGAGATCTACTAGGCTGCACGCTGATGAGAGGGA 918
 554 CTCACAAACAAAGTGTATATACAGAGAAAGAAAGATTTGTAGCTGTTTGCTTATC 613
 919 TTAACAAGCTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 978
 614 TTGAAAGAAAGCAAAAGCAAGTCTTAAAGTGTGCAAGCAAGCAAGCAAGTCTTCCG 673
 979 AGGTGTTGAGTGGCGGAGAGATTAATACCGGATCGGATCGGATCGGATCGGATCGG 1038
 674 AATTAAGAAATTTCTAGACATTTTTCAGTCTGTTGCTGCTTCCGTTTACGAAAG 733
 1039 AGTACATCCAGCATGAGATTCGTTGAGTGGCATGTGCGGCTGCTGTTAGCGCG 1098
 734 GAATATCTGATGATGATGATGAAACCTTCTTGTTGCTGAGAGTGTGCTACTAAG 793

Db

Db 940 ATTAAATGATGATATTTTGGTATAGTAAAGTTGCTTTCCATCAACTAACTAACTAAACATTT 999

QY 1293 AAGCAAAAAACAGATGCTTCTCTGATGCGGATGCTCAAGGACAGAGCGTAAGTTG 1352

Db 1000 AAGCATGTGGCGAAAACGTCATCTTACATTTAGT-----AAGACATTAAGAACGTAAAGCA 1050

QY 1353 AGCTGGGTGTGAGACGCTACACATACATACGTCGAGAAAGCATGTGCTATTTACCTGAA 1412

Db 1051 GTTTGGGATAAATGGATGATGAACAGATTTTGAATTAATGACAAATTCACCACTTACGTCAGAA 1110

QY 1413 TACGTTGCTCTATTTTGAACGAGCTGGCGGATGAAGAGTGGCGTATTACTGTGTGATACC 1472

Db 1111 CGTTAATGAAAGCAATCAATGCTAACTTAATAAGATGATGCAATTATCTCAGCAGATGTT 1170

QY 1473 GGCAATGTCATATGTGTGCGATGCCAGGTATCATCGAATTCGAGAGGAACGGCGACATT 1532

Db 1171 GGAATCTTACAGTATGGCTTACAGCGGTTACTTAAACTTATC---TGTAATAATTAATTTTC 1227

QY 1533 GTGGGTCATTTCCGCGACGACATGSCATATGCTGATGGCTCATGCGATTGGTGGCGAA 1592

Db 1228 ATTATTTCTAGTGGTATAGTACTATTTGGGCTGTGTTTACCAAGTGCATGGCAGCTAAA 1287

QY 1593 AGTGTGATCCAAACCGCCAGGTGATTCGGATGTGTGGCGATGCTGTGGGCAATGCTG 1652

Db 1288 ATTTGTTATCCAAACCGCCAGGATGATCTATCACAGGTGAGCGGCTGCCAATGCTA 1347

QY 1653 CTGGGTGAGCTTCTGACCGCTTAAGCTGACCAACTCTCCGCGAAGGCTGTGTGTTTAC 1712

Db 1348 ATGCAGACTTTGGCTACAGCTGTTCATATATACCTATACCAATGACATCTTGTATTAAT 1407

QY 1713 AACGATCTTTGGGCGATGTGTAAGTTGGAGATGCTCGTGAAGGACAGCCAGAAATTTG 1772

Db 1408 AACCAACATTTGTCTATTCATTTAAATATGACAAACAGCTGCTGGTAATTAGATATGCC 1467

QY 1773 ACTAACCATGAGGAAGTGAATTTGCGAGAGATTTGGGGGCTGTGGGGGTATCAATTCGTA 1832

Db 1468 ATGATTTTCTGTGATATGATGATCATGCTAAATTTGCTGAAGTGTGTTGGGTAAAGGCTAT 1527

QY 1833 CGCATCACCGATCCGAAGAAAGTTCCGGAGCAGCTAGCTGAGGCGATATGCTGTA 1892

Db 1528 GTTGTGAAGATGTGAGTGTCTGTCGACAAACATGCTGTAAGAGGCAATGGCTCAAGATGTT 1587

QY 1893 CCTTACTGATCGATATCGTACGAGATGCTTAATGCGCTGTGCGATCCCAACCAATCAGC 1952

Db 1588 CCAACATCTGTGACGTTCATGATGATCTTAATCTGTCGACCATTAACAGGTAAATATGTA 1647

QY 1953 TGGCAACAGTCATGAGATTCAGCAAGCGGC 1984

Db 1648 AACGAAAGACATTTGGTTACAGTAATATGGGC 1679

RESULT 7

US-09-252-991A-8458

Sequence 8458, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196, 136

CURRENT APPLICATION NUMBER: US/09/252, 991A

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074, 788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 8458

LENGTH: 2577

TYPE: DNA

ORGANISM: *Pseudomonas aeruginosa*

US-09-252-991A-8458

Query Match	Similarity	4.6%	Score 100.4	DB 4	Length 2577
Best Local	Similarity	45.5%	Pred. No. 7e-21		
Matches	773	Conservative	0	Mismatches 856	Indels 69
				Gaps	9
QY	327	ATGGCACACACACTACGACGAAACAATTAATTGACCTTTGGAAGCTCAAGTGTGAAGCA	386		
Db	805	ATGTCCACACAGGTTGGCCGATCAATTGCTCCGAACGCTTGAGCCAGTGGGGGTGAAGCCG	864		
QY	387	ATTATATGTTTGGTGGGTGACAGCCTTAATCCGATGTGATGCTGT-----CCGCCAA	440		
Db	865	GTCCTCGGCTCCCGAGCGATGCGATCAACGCGATCATGTGGCGCCATGGGCGCGCGCC	924		
QY	441	TCAGATATGAGTGGGTGACAGTTCGAAATGAGGAAGCGCGCGCTTTGACCGGTGCG	500		
Db	925	GAGCATTCCGACTATATCCGGGTGGGCCACGAGAGATGGCGCTTCATGCGCGCGCC	984		
QY	501	GAATCGTTGATCAGTGGAGAGCTGGCAGTATGTGCTTCTTGTGTGCTTGGAAACACA	560		
Db	985	CACGCCAAGTTCACCGAGAGAGTGGGGGTGTGCTCTGGCACCTCGGGGGCGGGGAGATC	1044		
QY	561	CACCTGATTCAGGCTCTTATGATTTCCATGCAATGTTGCGAAGGTGTTGGCCATGCT	620		
Db	1045	CACCTGCTGAACGGGCTCTTACAGCGCGGCAATGATATCATCACCGGCTGTGCTCATGTC	1104		
QY	621	AGCCATATTCGAGTGGCCAGATTTGTTGCGAGCTGCTTCACAGAAACGATCCGGAGTT	680		
Db	1105	GGCCACAGAGGGGCTACCGGCTTGGGACGACGACTACCAAGCAGAAAGTGTATGTCAGAC	1164		
QY	681	TTGTTTAAAGAAATGCTCTGTTTACTCGGAGATGTTGAATGTTGTGAGCAGGGTGAACG	740		
Db	1165	TTTGTTCAAGGACGTTTCCGCTATGTGAGACGCTGTGTCAGCCCGGACCAATGCTCTCAT	1224		
QY	741	ATTGTTGATCAGCGGATTCAGTTCACATACATGCGGGGTAAAGTGTGCTGCTGACTGAT	800		
Db	1225	GTTGTGACACGAGCCCTGCGGTGGCGGTGCGCGACGCGCAGGTGGCCAGGTGATCTGTG	1284		
QY	801	CTTGGTATATTCGCTAAGGAAGACGC---AGTGCACGCTACTTATTCATTTCCACTAT	856		
Db	1285	CCCAACAGCAGTGCACAGATGGCGGCCCGAAGGCGCCAGCCACAGACACGCGCACGTCG	1344		
QY	857	TTCCTTGGGACACTGCTGTGGTGTCCCGGATCTTA-----CTGAGGCTCAGACG	905		
Db	1345	ATGTGCGCGGTGGGCTTGTGTCCAGCCCGACCTTCACGCGCGACGCGCAGCTGTGAGGC	1404		
QY	906	CTGTGGAGAGCGATTAAACAACGCTATGCTGTCTTGTGCGTGGCGGAGCTGTGAAG	965		
Db	1405	GCGCGGCGATCTCTCAATCGCGGCGGGGTGGCGATCTCTGGCGCGTGGCGGCGCTG	1464		
QY	966	AATGCTTCGCGCGAGGTGTGGAGTGGCGGAGAAAGATTAAATACCGATCGGCATCGC	1025		
Db	1465	GCGCGCCACCGGACACTGGAAGCGGTGGCGAGGCGCTGTGCGCGCGGAGTGGCCAAAGCG	1524		
QY	1026	CTGGGTGGTAAAGAGTACATCCAGCATGAGAATTCGTTTGGTGGGTGCGGATGTGCGCTG	1085		
Db	1525	CTCTGGGGAAGGCGGGGTTTCCGAGACCTGCGTACGAGTGGCGGCTGCATGCGGCTG	1584		
QY	1086	CTTGTGTACGGCGCTCGGTGTGATGCGTCCATGAGGCGGATCTGCTGATTTCTATTGGGT	1145		
Db	1585	CTCGGCAACCGCGCCACGACACATGCTGATGAGAGCATGTGCACACACCTGATGTGTGCG	1644		
QY	1146	ACGAGATTCCTTATTTCTGATTTCTTCTTAAGACAAAGTTGGCGCAGGTGGATATCAAC	1205		
Db	1645	AGACATTTCCCTACAGCGAGTTCCTACCCAAAGGCGCGCCAGGCGGGCGGTGCAAGTTC	1704		
QY	1206	GGTGGC-----CACATTGGTCGACGTACCAAGGTGAAGTATCCGATGACCGGTGAT	1256		
Db	1705	GACCTGTATCCGGCAACAATCGGTATTCGGTATCCGATTCGACCGAGGCTTGTGCGGAT	1764		
QY	1257	GTTGTGCAACAATGCAAAATATTGTTGCCATGTAAGGAAAAAACAAGATCTTCCTTC	1316		
Db	1765	GCAGGGGAAACCTTGAGCGCGCTGCGCGCTCTCTGAGAGAAAAGACGCGGCT--	1822		
QY	1317	CTTGATCGGATGCTCAGGCACACGAGCGTAAATTGAGCTCGGGGTGAGAGACTACACA	1376		

Db 1823 -----GGCGCCGCGCGGTGAGCGGGGTGACGGCCAGTGGGAGGAAGCCGCGGC 1875
QY 1377 CATAAGTCGAGAACAGCATGTGCTATTCACCTGATACGTTGCTCTATTTTGAACGAG 1436
Db 1876 CAGGCCGAGAGACCGACCGCCGATACCCGACGAGCGGGTATTCGGTCTCTGTGCGG 1935
QY 1437 CTGGCGGATAGAGATGCGGTGTTTACTGTGATACGCGCATGGCAATGTGGCATGGG 1496
Db 1936 CAACTGCGGAGAGATGCGGATCTCTGCGGCGACAGCGGCTCCGATACCACTGCTGACGC 1995
QY 1497 AGGTACATGAGAAATCCGAGGAAACGCGCATTTGTTGATTCATTCGCCACGACGACG 1556
Db 1996 CCGCAGATCCGATCCGCGCCGCGCATGCTCGGCTCGCTG---TCGGGCAAGGTGGGAC 2052
QY 1557 ATGGCTAATGCTTCCCTCATGCGATTTGGTGGCAAGTGTGATGAAACCGCACGAGTG 1616
Db 2053 ATGGGCAAGGCGTCCCTACCGCATTCGCCCAAGCTCGCTATCCGAGGCGGCGGTG 2112
QY 1617 ATCGGATGTGTGGGATGTTGGATGCTGTGGATGCTGTGGAGCTTGTGACCGTTAG 1676
Db 2113 GTGGCGATGTGGGAGCGGCGCCCATGCAATGAACGCGACGCGCAACTGTGACCGGTG 2172
QY 1677 CTGCACCACTTCCG-----TGAAGGCTGTGTTTAAACAAGT 1718
Db 2173 CAGCAGTACTGCGACGCTGGGACTCGCCGACCTTCATCGTGTGCTGTGAACAACGCGC 2232
QY 1719 TCTTGGGCGATGATGAGTGTGAGATGCT---TCGTGAGAGGAGACCGCAAGATTTGTACT 1775
Db 2233 GATCTCAACCGAGGTACCTGGAGCAGCGTGCCTCGCGCGGACCGGAGTTCAGCCCG 2292
QY 1776 GACCATGAGGAAGTAAATTTGCGAGAG-----ATTGGCGGGCTGGCGGTATCAAAATG 1829
Db 2293 GCGCGAGAAATGATGATTTCCCTACGCGGCTTATGGGACATGCTGCGCTTCAAGGCG 2352
QY 1830 GTAGCATACCGATCCGAAGAAATTCGAGCAGTGAAGCATTTGGCATATCT 1889
Db 2353 ATCCGCGTGAATCGCCCGAGACATCGACCGCGCTGGCGGAGCGCTTGGCGCGCGAC 2412
QY 1890 GGACCTGACTGATGATATGATGTCACGAGATGCTATGCTGTGATCCACCAACCATC 1949
Db 2413 CGCCCGGTGCTGCTGGAGGTGTCAACGACCGAAGCGTCCGCGCTCCCGCACATC 2472
QY 1950 ACGTGGGAACAGGTCAAG 1967
Db 2473 AGTTTCGAGCAGGCCAAG 2490

RESULT 8

US-09-252-991A-8530
; Sequence 8530, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIORITY FILING DATE: 1999-02-18
; PRIORITY FILING DATE: 1998-02-18
; PRIORITY FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8530
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8530

Query Match 4.6%; Score 100.4; DB 4; Length 2754;
Best Local Similarity 45.8%; Pred. No. 7.2e-21;
Matches 773; Conservative 0; Mismatches 856; Indels 69; Gaps 9;

QY 327 ATGGCACACAGCTACCGACACAAATTAATTGACACTTTGGAAGCTCAAGCTGTGAACGA 386
Db 671 ATGTCCAGACAGGTTCCCTCCATTAATGCTGAACCGCTTGAGCCAGTGGGGGGAACCGC 730
QY 387 ATTATGATGTTGGTGGGTGACACACCTTAATCCATGTGATGCTGT-----CGCCAA 440
Db 731 GTCTTGGGCTACCCAGCGCATGCGATCAAGGGATATGGGCCCATGGCCCGCGCGCC 790
QY 441 TCAGATATTGAGTGGGTGACGCTTCAAAATGAGGAAGCGGGGCTTGGACCGCGGCG 500
Db 791 GAGGATTTGACTATATCCCGCTGGCCGACAGAGAAATGGCGGCTTCAATGGCGGCGCC 850
QY 501 GAATCGTTATCATCTGGGAGCTGGCAGTATGCTGCTTCTTGTGCTCTGGAACACA 560
Db 851 CAGCGCAAGTTCAACCGAGAGGTGGGGTGTGCTCGCCACGTCGGGGCGGCGGCATC 910
QY 561 CACCTCATTCAGGCTTTATATGTTGGCATCGAAATGTTGCGAAGTGTGGCCATCGT 620
Db 911 CACTGTCTAAGCGGCTTACGACGCGCGCATGATCATCAGCGGCTGCGCATCTGC 970
QY 621 ACCCATATTCCGAGTCCCGAGATTGCTGACGTTCTCCAGGAAACGATCCGGAGAT 680
Db 971 GGCCACAGGCGGCTACCGCGTTGGCAGCGACTACGACGAGAAATGCTGTGCAAGC 1030
QY 681 TTGTTTAAAGGAATGCTCTGTGTTACTGCGAGATGTGAATGTGTGAGCAGGCTGAACGC 740
Db 1031 TTGTTCAAGAGCTTCCGCTATGTCAGACCGTGTGACGCCCGGCACACATGCTCAT 1090
QY 741 ATTTCGATCAGCGGATTCAGTCCACATGCGCGGTTAAAGTGTGTGCTGTGATGAT 800
Db 1091 GTGTGAGACGAGCCCTGGCGTGGGGTGGGAGCGGACGCGAGTGGCGAGTGTGATGCTG 1150
QY 801 CCTGTGATATGCTTAAGSAGAACGC-----AGGTACGGTACTTATTCATTTCCACTAT 856
Db 1151 CCCAAGAGGTCAACAGATGCGGCGGCCGCGAGACGCCACCCACGACGACGCGCACGTG 1210
QY 857 TTCTTCTGGACTCTGTGTGTCTCCGATCTTA-----CTGAGGCTGCAAGC 905
Db 1211 ATGTGCGGCGTGGGTCTGTCAGCGCGACCTTACGCGCGGACCGACCTCGAGAGGC 1270
QY 906 CTGTGAGAGCGGATTAACAAAGCTAAGTGTGACCTTTTGTGCGGTGCGGCGGTGAAG 965
Db 1271 GCGCGGCGATCTTAATGCGCGCGCGGCGGAGTCTTGCAGGCTCCGCGCGCGCTG 1330
QY 966 AATGCTCGCGCGCAGGTGTGAGTGTGGCGGAGAAATTAATCAACCGATCGGCGATGCG 1025
Db 1331 GCGCGGCAACGCGCACTGGAACCGGTCCGCGAGCGCGCTGGCGGAGTGGCCAAAGCG 1390
QY 1026 CTGGGTGTAGCAGTACATCCAGCATGAGAAATCGTTGAGGTGCGCATGTCGTGCGCTG 1085
Db 1391 CTGCTGGGCAAGCGCGGCTTCCGACGACCTGCGGTACGTGACCGGCTCCATCGGCGCTG 1450
QY 1086 CTGTGTACGGGCGCTGTGGTGTGATGCTGATGAGGGGATCTGCTATTTATTTGGGT 1145
Db 1451 CTGGGACCGCGCGGAGCAGCATGCTGATGAGGCAATTCGACACCTGCTGATCTGCGC 1510
QY 1146 ACGATTTCCCTTATTCGATTTCTTCTTAAGACAAGTGTGCCAGGTGATATCAAC 1205
Db 1511 AGCACTTCCCTTACAGGAGTCTCTACCGAAGGCGCGGCGAGCGCGGTGCAGATC 1570
QY 1206 GGTGCG-----CACATTGCTGACGTACCAACGAGTGAATCCGCTGACCGGTGAT 1256
Db 1571 GACCTGTATCCGCGCAGCATGCTATCCGATATCGATGACACAGGCTTGTGCGCGAT 1630
QY 1257 GTTGTCGACACATCGAATAATATTTGGCTCATGTGAAGGAAAAACAGATCTGCTTTC 1316
Db 1631 CAGAGGGAACCTCTGAGCGCGCTGCTGCTGCTGCGAGCAAGAAAAACAGCGCCCT-- 1688
QY 1317 CTGTAGCGATGCTCAAGGCAACAGAGGTGATGAGCTGCTGCTGTGATGACATCA 1376
Db 1689 -----GGCGCGCGCGGTGACGCGGCGGTGAGCGGCATCGGAGAGGAAGCCGCGCGC 1741

```

/ ATTORNEY/AGENT INFORMATION:
/ NAME: FLOYD, LINDA A.
/ REGISTRATION NUMBER: 33,692
/ REFERENCE/DOCKET NUMBER: CR-9989
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 302-892-8112
/ TELEFAX: 302-773-0164
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 260 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ ORIGINAL SOURCE:
/ STRAIN: dpd3509 lower
/
US-08-735-545-24

Query Match 4.0%; Score 87.2; DB 3; Length 260;
Best Local Similarity 58.5%; Pred.No.2.7e-17;
Matches 152; Conservative 0; Mismatches 108; Indels 0; Gaps 0

QY 471 GAGGAAGCGGGCGCGTTGGCAAGCCGGTGGGAATCGTGAATCACTGGGAGCTGGCACTA
Db 260 GAGGAAGTGGGGCGCTTTGGCCGCGCGCCCTGAAGACAACTAGCGAGAACTGGCGGTC
QY 531 TGTGCTGCTTTTGTGTGTCCTGGAACACACACCGATTACAGGTCCTTATGATTGCGAT
Db 200 TGGCGGGATGTGTGGGGCCCGCGGCACTGCACTTAATCAAGCGCTGTGGATTGGCAC
QY 591 CGAATAGTGGGAAGTGTGTGGCATGCGTACCATATTCGATTCGAGTGGCCAGATTGGTTCG
Db 140 CGCAATACAGTTCGCGTACTGCGCATTTGCCCTCATATTTCCTCAGGAATTTGGCAGC
QY 651 ACGTATCTCCAGGAACGACATCCGAGATTTTGTTAAGAAATGCTCTGGTATTCGCGAG
Db 80 GCGATTTCCAGGAACCCACCAAGACTATTCCGGAATGTAGTACTATTGGCAG
QY 711 ATGCTGAATGTGTGTAGCA 730
Db 20 CTGGTTCCAGCCCGGAGCA 1

RESULT 10
US-09-083-24/c
/ Sequence 24, Application US/09449083
/ Patent No. 6194159
/ GENERAL INFORMATION:
/ APPLICANT: Van Dyk, Tina K.
/ TITLE OF INVENTION: A Facile Method for
/ TITLE OF INVENTION: Identifying Regulated
/ NUMBER OF INVENTIONS: 28
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: E. I. DU PONT DE NEMOURS
/ ADDRESSEE: AND COMPANY
/ STREET: 1007 MARKET STREET
/ CITY: WILMINGTON
/ STATE: DELAWARE
/ COUNTRY: UNITED STATES OF AMERICA
/ ZIP: 19898
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: DISKETTE, 3.50 INCH
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: MICROSOFT WINDOWS 3.1
/ SOFTWARE: MICROSOFT WORD 2.0C
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/449,083
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: FLOYD, LINDA A.

```


	Query Match	Score	DB	Length
	Similarity	%	No.	(bp)
Best local	52.3%	Pred.	5e-15*	1443
Matches	Conservative	0;	Mismatches	183; Indels 6; Gaps 1
QY	327 ATGGCACACAGCTGACGAACAATTATTTGACACTTGTGGAACTCAAGTGTAAGCCA	386		
Dh	864 ATTGCCACAGCAGGTTGCCGATCAATTCTCGAAGCGTTGACCACATGGGGGGGTGAAGCCC	805		
QY	387 AATTATGGTTTTGGTGGGTGAACGCCTTAATCCCATGTGAGATGCTGT-----CCGCCAA	440		

LOCATION: 951..1032
FEATURE:

NAME/KEY: CDS
LOCATION: 1195..2838
US-08-452-075-1

Query Match 2.8%; Score 60.8; DB 2; Length 2841;
Best Local Similarity 45.8%; Pred. No. 1.7e-08;
Matches 209; Conservative 0; Mismatches 247; Indels 0; Gaps 0;

341 CGCAGAACATTAATGACATTTGGAACCTCAAGCTGAGGCAATTATGTTGGT 400
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
1203 CGCAGAGTGGTGGTACATCGCTTGGGGCACAAGGTGTGAACACCGTTTGGTTATCC 1262
401 GGGTGACAGCTTAAATCGATCGTGGATCTCTCGCCCAATGATATTGAGTGGTGA 460
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
1263 GGGTGGCGCAATTAATCCGTTTACGATGATGATACGGCGCGGTGAGACCACTTGT 1322
461 CGTTGCAATGAGGAGCGCGCGCTTTCACCCGGTGGGAATGATGATCACTGGGA 520
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
1323 ATGCCCAATGAGCAGAGGAGGCGCAATGCGGCTATCGTTATGCTCGCTACCGGCA 1382
521 GCTGAGATATGCTGCTCTTGTGTCCTGGAACACACACCTGATTCAGGGTCTTTA 580
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
1383 AACTGGCATATGATGATCGCCACGCTGTGTCGGGCGCAACCACTGATTAACGGGCTTGC 1442
581 TGATTCGACATCGAAATGAGTGGCAAGGTGTGGCCATCGCTACCATATTCGAGGCCCA 640
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
1443 GGACGCACTGTATGATTCATCCCTCTTGTTCGATCACCCTGATGCTCCGACCGTT 1502
641 GATTGCTGACCTTCTCCAGCAACGCAATCCGAGATTTGTTAAGAAATGCTCTGG 700
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
1503 TATCGGCACTGACGATTCAGAGAGTGAATGCTGGGATTTGCTTACCTGTACCA 1562
701 TTACTGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 760
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
1563 GCATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1622
761 GTCCACCATGCGCGGTAAGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 796
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
1623 CGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1658

RESULT 13
US-09-231-061-1
Sequence 1, Application US/09231061
Patent No. 6214591
GENERAL INFORMATION:
APPLICANT: TOMITA, FUSAO
APPLICANT: YOKOTA, ATSUSHI
APPLICANT: HASHIGUCHI, KENICHI
APPLICANT: ISHIGOKA, MASAKO
APPLICANT: KURAHASHI, OSAMU
TITLE OF INVENTION: METHODS FOR PRODUCING L-VALINE AND
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATR & NEUSTADT,
STREET: 1755 S. JEFF. DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,061
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/793,441

FILING DATE: 28-FEB-1997
APPLICATION NUMBER: PCT/JP95/01719
FILING DATE: 30-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-204856
FILING DATE: 30-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-843-0 PCT
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2841 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: ESCHERICHIA COLI
STRAIN: M162
FEATURE:
NAME/KEY: CDS
LOCATION: 957..1055
OTHER INFORMATION: /note="IDENTIFICATION METHOD: S"
FEATURE:
NAME/KEY: attenuator
LOCATION: 1081..1104
OTHER INFORMATION: /note="IDENTIFICATION METHOD: S"
FEATURE:
NAME/KEY: CDS
LOCATION: 1195..2841
OTHER INFORMATION: /note="IDENTIFICATION METHOD: S"
FEATURE:
NAME/KEY: misc-feature
LOCATION: 52..57
OTHER INFORMATION: /note="CLEAVAGE SITE: SmaI,
OTHER INFORMATION: IDENTIFICATION METHOD: S"
FEATURE:
NAME/KEY: misc-feature
LOCATION: 2395..2400
OTHER INFORMATION: /note="CLEAVAGE SITE: KpnI,
OTHER INFORMATION: IDENTIFICATION METHOD: S"

Query Match 2.8%; Score 60.8; DB 3; Length 2841;
Best Local Similarity 45.8%; Pred. No. 1.7e-08;
Matches 209; Conservative 0; Mismatches 247; Indels 0; Gaps 0;

341 CGCAGAACATTAATGACATTTGGAAGCTCAAGGTGTGAAGCAATTATGTTGGT 400
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
1203 CGCAGAGTGGTGGTACATCGCTTGGGGCACAAGGTGTGAACACCGTTTGGTTATCC 1262
401 GGGTGACAGCTTAAATCGATCGTGGATCTCTCGCCCAATGATATTGAGTGGTGA 460
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
1263 GGGTGGCGCAATTAATCCGCTTACGATGATGATGATGATGATGATGATGATGATGAT 1322
461 CGTTGCAATGAGGAGCGCGGCTTTCACCCGGTGGGAATGATGATCACTGGGA 520
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
1323 ATGCCCAATGAGCAGAGGAGGCGCAATGCGGCTATCGTTATGCTCGCTACCGGCA 1382
521 GCTGAGATATGCTGCTCTTGTGTCCTGGAACACACACCTGATTCAGGGTCTTTA 580
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
1383 AACTGGCATATGATGATCGCCACGCTGTGTCGGGCGCAACCACTGATTAACGGGCTTGC 1442
581 TGATTCGACATCGAAATGAGTGGCAAGGTGTGGCCATCGCTACCATATTCGAGTGGCA 640
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
1443 GGACGCACTGTATGATTCATCCCTCTTGTTCGATCACCCTGATGCTCCGACCGTT 1502

QY 641 GATGGCTTGCACGCTTCTTCCAGAAAGGCAATCCGAGATTTTGTTTAAGCATGCTCTGG 700
Db 1503 TATGGCAGTCAGCCATTTTCAAGAAAGTGAGATGTCCTGAGATTGCTGTAGCTGTACCA 1562
QY 701 TTACTGCGAGATGGTGATGATGATGAGACAGGGTGAAGCATTTTGCATCAGCGATTCA 760
Db 1563 GCATAGCTTTCTGGTGGAGTGGCTGTGAAGATTTGCCGCGCATCATGCTGAAGCATTCGA 1622
QY 761 GTCCACCATTGGCGGATTAAGGTGTGTCGGTGGTGTAGT 796
Db 1623 CGTTGCCCTCCTCAGGTGCTCCTGGTCCGGATTCTGGT 1658

RESULT 14

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1 / S-09-011-762-5
2 / Sequence 5, Application US/09011762
3 / Patent No. 6319696
4 / GENERAL INFORMATION:
5 / APPLICANT: KISHINO, Hiroko
6 / APPLICANT: KISHINO, Hiroko
7 / APPLICANT: IZUI, Masako
8 / APPLICANT: ONO, Yukiko
9 / APPLICANT: ITO, Hisao
10 / APPLICANT: KURAHASHI, Osamu
11 / TITLE OF INVENTION: METHOD FOR PRODUCING L-AMINO ACID
12 / FILE REFERENCE: 0010-0911-OpCT
13 / CURRENT APPLICATION NUMBER: US/09/011,762
14 / EARLIER FILING DATE: 1998-04-17
15 / EARLIER APPLICATION NUMBER: PCT/JP96/02359
16 / EARLIER FILING DATE: 1996-08-27
17 / NUMBER OF SEQ ID NOS: 11
18 / SOFTWARE: PatentIn Ver. 2.0
19 / SEQ ID NO 5
20 / LENGTH: 2841
21 / TYPE: DNA
22 / ORGANISM: Escherichia coli
23 / FEATURE:
24 / NAME/KEY: CDS
25 / LOCATION: (957)..(1055)
26 / FEATURE:
27 / NAME/KEY: CDS
28 / LOCATION: (1081)..(1104)
29 / FEATURE:
30 / NAME/KEY: CDS
31 / LOCATION: (1195)..(12841)
32 / FEATURE:
33 / NAME/KEY: misc_feature
34 / LOCATION: (52)..(57)
35 / OTHER INFORMATION: cleavage site (SmaI)
36 / FEATURE:
37 / NAME/KEY: misc_feature
38 / LOCATION: (2395)..(2400)
39 / OTHER INFORMATION: cleavage site (KpnI)
40 / S-09-011-762-5

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Query Match	2.88;	Score 60.8;	DB 4;	Length 2841;
Best Local Similarity	45.88;	Pred. No. 1.7e-08;		
Matches 209;	Conservative	0;	Mismatches 247;	Indels 0;
			Gaps	0;

OY	341	CCACAGAACAAATTAATTGACACTTTGGAAAGCTCAAGGTGTAAAGCAAATTATGCTTGGT	400
Dd	1203	CGCACAGTGGTGTCATACCGCTGGCGGACAGGGGTATAACAACCCTTTTGGGTATACC	1262
OY	401	GGGTGCACGCCCTTAATCCGATCCTGGATGCTGTCCGCACATCATGAATTAATAGTGGGTGCA	460
Dd	1263	GGGTGGCCCAATTATATCCGGTTTAGCATGATCTGTATGACGGCGCGGTGGACGACTTGGT	1322
OY	461	CGTTGCAATTAGAGGAAGCGCGCGCTTTTGCAGCCGGTGCAGGAATCGTTGATCACTCGGGA	520
Dd	1323	ATGCCGACATAGCAGCGGTGCGGCATATGGCGCTATACGGTTATGTCTGTCTACCCGCCA	1382
OY	521	GCTGGCAGATGCGCGCTTTCTTGTGTGCTCTGGAAACACACACACTGATTAGGGTCTTTA	580
Dd	1383	AAC TGCGGATATATACGCCACGCTGTGTGCTCGGGCGCACACCACTATTAACCCGGGCTTGC	1442

QY	581	TGATTGCATCGGAATGTTGGGAAGGTTGGCCATGCTTCGCATATTCGCAGTGGCCA	640
Db	1443	GGAGCGACATGTTAAATTCATCCTCTGTTGTGGCATACGGGTCAAGTGTGCGACCGTT	1502D
QY	641	GATTGGTTGCAGCTTCTTCGAGGAAGCATCCGGAATTTGTTAAAGAAATGCTCTGG	700
Db	1503	TATCGGCACAGCCGATTTTCGAGAAAGTGAAGTGTCTCTGGATTTGTCTGTTAGCTGTACCA	1562D
QY	701	TTACTGCGAGATGTTGAATGGTGTGAGCAGAGGTGAAGCGCATTTTTCATCAGCGGATTTCA	760
Db	1563	GCAATAGCTTTTGGTGCAGTCGCTGGGAAGAGATTTCCCGCGCATATCATGGCTGAAGCATTTGA	1622D
QY	761	GTCACCATGGCGGGTAAAGGTGTGTCGAGTGATGT	796
Db	1623	CGTTGCTCTGTCAGAGTGTCTCTGGTTCGCGGTTCTGGT	1658D

RESULT 15

```

US-08-961-527-48/C
; Sequence 48, Application US/08961527
; Patent No. 6420135
;
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 25002 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
IS-08-961-527-48

```

Query Match	2.83	Score 59.8	DB 4	Length 25002
Best Local Similarity	46.28	Pred. No. 11e-07		
Matches 236	0	Mismatches 272	Indels 3	Gaps 1

QY	343	CGAGAACAAATTAATTGACACTTTTGGAGCTCAAGGTGAGAGCGAATTTATGTGTTGGTGG	402
QY	6437	CTCCAGCAATAGCTTAAAGCTATTTAAACAAATGGGGCGTAGATACATCTACGGTATCCCAT	6378
QY	403	GTGACAGCCTTAATCCGAGTCGTGAGTCTGTCCGCCAA--TCGAATATTAGTGGGGTGC	459
QY	6377	CAGGAACACTCACTATTGATGATGAGACCTTTGGCTGGAAGACAAAGAGATATCCGTTCTTAC	6318
QY	460	ACGTTTCGAATGAGAGAGCGGGCGGCTTTCACGGCGGTGGGGAATCCTTGATCTACTGGGG	519

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Db      6317 AAGTTGCGCCAGGAGACAGGTGCTTTCAGACGGTATGCAAGCTAAATTGCGCGCT 6258
QY      520 AGCTGGCAGTATGCTGCTCTTGTGTCCTGAAACACACACCTGATTCAGGGTCTT 579
Db      6257 CAATCGGGGTGAGTGTGTCAGGTGTCAGGTGCGACTGACTGATTAAGGTGTT 6198
QY      580 ATGATTGCGCATCGAAATGTTGCGAAGTGTGGCCATGCGCTAGCCATATTCGAGTCCC 639
Db      6197 ACGATGCACTATGATTAACACTCCATTCCTAGCGATCCTTGATCAGCTCCAGTTAACG 6138
QY      640 AGATTGGTTCAGCTCTTCCAGSAAACGATCCGGAGATTTGTTAAGSAAATGCTCG 699
Db      6137 AATTGAACATGATGCTTTCACAGCTTAACCAAAACCAATGTACAAAGGTATGCTG 6078
QY      700 GTTACTGCGAGATGTGAATGTGTGAGCAGGAGTGACGATTTGCATCAGCGATTC 759
Db      6077 TTTACAAACAACGTGAGCTTACGTAGCAATTGCCAAAGTAATTGACGAAGCCTGCC 6018
QY      760 AGTCCACCATGGCGGGTAAAGTGTGTGCTGATGATTCCTGATATCGCTAAGG 819
Db      6017 GTGCTGCAGTTTCTTAAAAAAGTCCAGCTGTGTGAATTCAGTAAACTTCGGTTCC 5958
QY      820 AAGACGAGGTGACGAGTACTTATTCCAATTC 850
Db      5957 AAGAAATGATGAATACTACTACGTTTC 5927
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Search completed: October 3, 2003, 18:52:48
Job time : 164 secs

GenCore version 5.1.6
(c) 1993 - 2003 Compu

18

6 ; Search time 563 Seconds

10356.636 Million cell updates/sec

.....gtgtcccatgagattgccct 2160

5

/g/genseq-n-emb1/NA1980.DAT.*	/g/genseq-n-emb1/NA1981.DAT.*	/g/genseq-n-emb1/NA1982.DAT.*	/g/genseq-n-emb1/NA1983.DAT.*	/g/genseq-n-emb1/NA1984.DAT.*	/g/genseq-n-emb1/NA1985.DAT.*	/g/genseq-n-emb1/NA1986.DAT.*	/g/genseq-n-emb1/NA1987.DAT.*	/g/genseq-n-emb1/NA1988.DAT.*	/g/genseq-n-emb1/NA1989.DAT.*	/g/genseq-n-emb1/NA1990.DAT.*	/g/genseq-n-emb1/NA1991.DAT.*	/g/genseq-n-emb1/NA1992.DAT.*	/g/genseq-n-emb1/NA1993.DAT.*	/g/genseq-n-emb1/NA1994.DAT.*	/g/genseq-n-emb1/NA1995.DAT.*	/g/genseq-n-emb1/NA1996.DAT.*	/g/genseq-n-emb1/NA1997.DAT.*	/g/genseq-n-emb1/NA1998.DAT.*	/g/genseq-n-emb1/NA1999.DAT.*	/g/genseq-n-emb1/NA2000.DAT.*	/g/genseq-n-emb1/NA2001B.DAT.*	/g/genseq-n-emb1/NA2002.DAT.*	/g/genseq-n-emb1/NA2003.DAT.*
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redicted by chance to have a core of the result being printed, tal score distribution.

IES

	Description
1	C. glutamicum genome
2	Corynebacterium g
3	Nucleotide sequen
4	C. glutamicum ATCC
5	Corynebacterium po
6	Corynebacterium p
7	C glutamicum codin
8	Corynebacterium g

C. glutamicum codi
Corynebacterium gl
C. glutamicum pyru
PCR product of C.
Nucleotide sequenc
C. glutamicum ATCC
Corynebacterium po
Corynebacterium gl
Propionibacterium
salmonella typhi D
Corynebacterium po
E. coli DNA for ce
Escherichia coli p
C. glutamicum codin
Corynebacterium gl
Escherichia coli p
Escherichia coli p
DNA encoding novel
Staphylococcus aur
Pathogen specific
Staphylococcus aur
Staphylococcus aur
Human ORX polynuc
Human ORX polynuc
Listeria innocua
Listeria innocua
Bacillus lichenif
Listeria monocytoc
C. glutamicum tran
Staphylococcus epi
Pseudomonas aerugi
Genomic sequence #
Genomic sequence
E. coli promoter re
Sulfolobus mehy
C. glutamicum deri
Oligonucleotide fo

MENTS

mal nutrition
case; pox.

PI Dunleau LK, McCormack A, Stapleton C, Burke K, Moeckel B:
PI Thierbach G.

XX
DR MPI: 2001-656800/75.
DR P-PSDB: AAU10194.

XX Preparation of L-amino acids, e.g. L-lysine, L-threonine or
PT L-isoleucine, useful in animal nutrition or in human medicine,
PT comprises fermenting L-amino acid-producing coryneform bacteria with
XX amplification of the tkt gene -

PS Example 6; Page 43-46; 53pp; English.

XX
XX The invention relates to the preparation of L-amino acids comprising
CC fermenting L-amino acid-producing coryneform bacteria which
CC overexpresses a gene e.g. that for transketolase, tkt. Also
CC included are transformed coryneform microorganisms harbouring the
CC plasmid ptc-118mb2 which contains the tkt gene. The method is useful for
CC the fermentative preparation of L-amino acids, i.e. L-lysine, L-threonine
CC and L-isoleucine, in which at least the tkt gene is amplified. L-lysine,
CC L-threonine and L-isoleucine are useful in animal nutrition. In human
CC medicine and in the pharmaceuticals industry. The present sequence
CC is the gene for pyruvate oxidase, poxh, which was eliminated by mutation
CC in a strain expressing with tkt in order to further increase yields of
XX L-amino acids.

XX Sequence 2160 BP; 491 A; 486 C; 647 G; 536 T; 0 other;

Query Match 100.0%; Score 2160; DB 22; Length 2160;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGAGCGATCTGTGAGTCACTTTTGGGGGCGGCTAAATTTGGCCACTTT 60
DB 1 TTAGAGCGATCTGTGAGTCACTTTTGGGGGCGGCTAAATTTGGCCACTTT 60
QY 61 CGAGCGACCAACAGAGCGGTGCCAGATGTTTAAATAGCGATGCGGATCTGT 120
DB 61 CGAGCGACCAACAGAGCGGTGCCAGATGTTTAAATAGCGATGCGGATCTGT 120
QY 121 TTGGTTGACGGGGTGAACCAACAGACTGCCACAGACGAGAAATCCCAAAAGT 180
DB 121 TTGGTTGACGGGGTGAACCAACAGACTGCCACAGACGAGAAATCCCAAAAGT 180
QY 181 GGGCATCCCTGTTTGGTACCGAGTACCCAGCCGCGCTGAAATCCTCTGGAGCGGGG 240
DB 181 GGGCATCCCTGTTTGGTACCGAGTACCCAGCCGCGCTGAAATCCTCTGGAGCGGGG 240
QY 241 AAGCGTGGCAACACTGGAATTTAAGACACAAATTGAAGTGGACCAAGTTAGGCAAC 300
DB 241 AAGCGTGGCAACACTGGAATTTAAGACACAAATTGAAGTGGACCAAGTTAGGCAAC 300
QY 301 AATAGCCATAGCTTGAAGGTGATGAGTACAGTACGACAGTACGACAAATTAATTGACA 360
DB 301 AATAGCCATAGCTTGAAGGTGATGAGTACAGTACGACAGTACGACAAATTAATTGACA 360
QY 361 CTTTGGAAAGTCAAGGTGGAAGCGAATTTATGTTGGTGGTGACACCTTAATCCGA 420
DB 361 CTTTGGAAAGTCAAGGTGGAAGCGAATTTATGTTGGTGGTGACACCTTAATCCGA 420
QY 421 TCGNGAGTCTGTCCCGCAATCATATATTGAGTGGGTGCAAGTTGAAATAGAGAAAGCG 480
DB 421 TCGNGAGTCTGTCCCGCAATCATATATTGAGTGGGTGCAAGTTGAAATAGAGAAAGCG 480
QY 481 CGGGGTTTGCAGCGGTGCGGAATGCTGATCAGTGGGAGCTGGAGTATGCTGCTT 540
DB 481 CGGGGTTTGCAGCGGTGCGGAATGCTGATCAGTGGGAGCTGGAGTATGCTGCTT 540
QY 541 CTTTGGTCTGGAACACACACTGATTCAGGGCTTTATGATTCGATCGAAATGCTG 600
DB 541 CTTTGGTCTGGAACACACACTGATTCAGGGCTTTATGATTCGATCGAAATGCTG 600
QY 601 CGAAGGTGTGGCATGCTAGCATATTCGAGTGGCCAGATTTGGTTCGAGTCTTCC 660

DB 601 CGAAGGTGTGGCATGCTAGCATATTCGAGTGGCCAGATTTGGTTCGAGTCTTCC 660
QY 661 AGGAAGCATCCGAGATTTTGTAAAGAAAGTCTGTGTTACTGAGATGTAATG 720
DB 661 AGGAAGCATCCGAGATTTTGTAAAGAAAGTCTGTGTTACTGAGATGTAATG 720
QY 721 GTGTGAGAGGTTGAACGCAATTTGATCAGCGATGATGTCACCATGCGGTAAG 780
DB 721 GTGTGAGAGGTTGAACGCAATTTGATCAGCGATGATGTCACCATGCGGTAAG 780
QY 781 GTGTGAGGTTGAGTATTCCTGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 GTGTGAGGTTGAGTATTCCTGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 ATTCCATTCACATATTTCTTGGCACTCTGTGTTCCCGATTCCTAGAGCTG 900
DB 841 ATTCCATTCACATATTTCTTGGCACTCTGTGTTCCCGATTCCTAGAGCTG 900
QY 901 CAGCGCTGTGAGCGGATTAACACAGCTAAGTCTGATGTTCTGCGGTGCGGCG 960
DB 901 CAGCGCTGTGAGCGGATTAACACAGCTAAGTCTGATGTTCTGCGGTGCGGCG 960
QY 961 TGAAGATGCTGCGCGGAGTGTGAGATGAGTGTGAGGAGAAATTAATCAACGATGCGG 1020
DB 961 TGAAGATGCTGCGCGGAGTGTGAGATGAGTGTGAGGAGAAATTAATCAACGATGCGG 1020
QY 1021 ATGCGCTGGTGTGAAGAGTACATCAGATGAGATGAGTGTGAGTGTGAGTGTG 1080
DB 1021 ATGCGCTGGTGTGAAGAGTACATCAGATGAGATGAGTGTGAGTGTGAGTGTG 1080
QY 1081 GCCTGCTGTGTTACGCGGCTGCTGAGATGCTGCAATGAGCGGATGCTGATCTAT 1140
DB 1081 GCCTGCTGTGTTACGCGGCTGCTGAGATGCTGCAATGAGCGGATGCTGATCTAT 1140
QY 1141 TGGGTAAGGATTCCTTATTCGATTCCTTCTTAACAAACAGTGGCCAGGTGATA 1200
DB 1141 TGGGTAAGGATTCCTTATTCGATTCCTTCTTAACAAACAGTGGCCAGGTGATA 1200
QY 1201 TCAACGGTGGCACAATTGGTGCAGTACACAGGTGAAGTATCCGGTGCAGGTGATGTT 1260
DB 1201 TCAACGGTGGCACAATTGGTGCAGTACACAGGTGAAGTATCCGGTGCAGGTGATGTT 1260
QY 1261 CTGCAACAATCGAAATATTTTGGCTCATGTAAGGAAAAACAGATGCTCTCTT 1320
DB 1261 CTGCAACAATCGAAATATTTTGGCTCATGTAAGGAAAAACAGATGCTCTCTT 1320
QY 1321 ATGCGATGCTCAAGCAGACAGAGCGTAAGTGAAGTGGTGAAGAGATGATACACATA 1380
DB 1321 ATGCGATGCTCAAGCAGACAGAGCGTAAGTGAAGTGGTGAAGAGATGATACACATA 1380
QY 1381 ACGTGCAGAGCATGTGCTTATTCACCGTGAATAGCTTCTCTATTTGAAGAGAGCT 1440
DB 1381 ACGTGCAGAGCATGTGCTTATTCACCGTGAATAGCTTCTCTATTTGAAGAGAGCT 1440
QY 1441 CGGATAGGATGCGGTTTACTGTGAGTACCGGATGCAATGTGTGCGATGCGAGGT 1500
DB 1441 CGGATAGGATGCGGTTTACTGTGAGTACCGGATGCAATGTGTGCGATGCGAGGT 1500
QY 1501 ACATGAGAAATCCGAGGAAACGCGCACTTGTGGTTCATTCGCCACGACAGATG 1560
DB 1501 ACATGAGAAATCCGAGGAAACGCGCACTTGTGGTTCATTCGCCACGACAGATG 1560
QY 1561 CTAATGCGTGTGCTCATCGATGCTGCGCAAAAGTGTGATGAAACCGCCAGGTATG 1620
DB 1561 CTAATGCGTGTGCTCATCGATGCTGCGCAAAAGTGTGATGAAACCGCCAGGTATG 1620
QY 1621 CGATGTGGGAGTGTGTTGGGATGCTGCTGGTGAAGTGTGACCTTTAAGCTG 1680
DB 1621 CGATGTGGGAGTGTGTTGGGATGCTGCTGGTGAAGTGTGACCTTTAAGCTG 1680
QY 1681 ACGAATTCGCTAAGAGCTGTGTTTAAACACAGTCTTTGGGATGAGTGTG 1740


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Db      781 GTGTGTGGTGTGATTCCTGTGTATTCGCTAAGGAAGCAGGTGACGGTACTT 840
QY      841 ATTCGAATTCACATATTTCTTCTGTGCACCTCTGTGTGTCCGGATCTACTGAGCTG 900
Db      841 ATTCGAATTCACATATTTCTTCTGTGCACCTCTGTGTGTCCGGATCTACTGAGCTG 900
QY      901 CAGCGCTGTGTGAGGCGATTAACAACGCTAGTGTCTGCTACTTGTCTGCGGTGCGGCG 960
Db      901 CAGCGCTGTGTGAGGCGATTAACAACGCTAGTGTCTGCTACTTGTCTGCGGTGCGGCG 960
QY      961 TGAAGATGTCTGCGGCGAGGTGTGAGTGTGCGGAGAGATTAATCACCAGATCGGCG 1020
Db      961 TGAAGATGTCTGCGGCGAGGTGTGAGTGTGCGGAGAGATTAATCACCAGATCGGCG 1020
QY      1021 ATGCGCTGGGTGTGAAGCAGTACATCCAGCATGAGAAATCCGTTTGGATGCGCATGCTG 1080
Db      1021 ATGCGCTGGGTGTGAAGCAGTACATCCAGCATGAGAAATCCGTTTGGATGCGCATGCTG 1080
QY      1081 GCGCTGTGTGTACGCGGCTGTGCGGTGTGAGTGTGCGCAATGAGGCGGATCTGCTAT 1140
Db      1081 GCGCTGTGTGTACGCGGCTGTGCGGTGTGAGTGTGCGCAATGAGGCGGATCTGCTAT 1140
QY      1141 TGGGTACGGAATTCCTTATTCGTGATTCCTTCTCTAAAGACAGCTTGCAGGTGATA 1200
Db      1141 TGGGTACGGAATTCCTTATTCGTGATTCCTTCTCTAAAGACAGCTTGCAGGTGATA 1200
QY      1201 TCACGCTGTGTGCACATTTGTGTGACGTACACGCTGTAAGTATCCGTTGACCGTATGTTG 1260
Db      1201 TCACGCTGTGTGCACATTTGTGTGACGTACACGCTGTAAGTATCCGTTGACCGTATGTTG 1260
QY      1261 CTGCAACAATCGAAAAATATTTTGCCTCATGTGAAAGAAAAACAATGCTTCTCTCTG 1320
Db      1261 CTGCAACAATCGAAAAATATTTTGCCTCATGTGAAAGAAAAACAATGCTTCTCTCTG 1320
QY      1321 ATGCGATGTCTCAAGGACACAGAGCGTATGCTGCTGTGTAGAGAGTACACACATA 1380
Db      1321 ATGCGATGTCTCAAGGACACAGAGCGTATGCTGCTGTGTAGAGAGTACACACATA 1380
QY      1381 AGCTGAGAGAGATGTGCTTATTCACCTGAAATGAGTGTGCTCTTATTTTGAACGAGCTG 1440
Db      1381 AGCTGAGAGAGATGTGCTTATTCACCTGAAATGAGTGTGCTCTTATTTTGAACGAGCTG 1440
QY      1441 CCGATTAAGAGTCCGCTGTTTACTGTGTGATACCGCATGTGCAATGTGTGCGATGCGAGT 1500
Db      1441 CCGATTAAGAGTCCGCTGTTTACTGTGTGATACCGCATGTGCAATGTGTGCGATGCGAGT 1500
QY      1501 ACATCGAGATCCGGGAGGAGGAGCGGATTTGTGGTTTCAATTCGCCACCGGACGATGG 1560
Db      1501 ACATCGAGATCCGGGAGGAGGAGCGGATTTGTGGTTTCAATTCGCCACCGGACGATGG 1560
QY      1561 CTAAATCGTGTGCTCATGTGATTTGTGCGAAAGTGTGTGATGAAACCGCCAGGTGATCG 1620
Db      1561 CTAAATCGTGTGCTCATGTGATTTGTGCGAAAGTGTGTGATGAAACCGCCAGGTGATCG 1620
QY      1621 CCAATGTGTGCGATGTGTGTGGGAGTGTGCTGTGGTGAAGTGTGACCTGTAGAGCTG 1680
Db      1621 CCAATGTGTGCGATGTGTGTGGGAGTGTGCTGTGGTGAAGTGTGACCTGTAGAGCTG 1680
QY      1681 ACCAATTCCTCGGTGAAGGCTGTGTGTATTAACAGAGTCTTTGGGCAATGTGTGAAGTTGG 1740
Db      1681 ACCAATTCCTCGGTGAAGGCTGTGTGTATTAACAGAGTCTTTGGGCAATGTGTGAAGTTGG 1740
QY      1741 AGATGTGTGTGAGGAGGACGCAAGATTTGTGTGATGACCATATGAGAGTGAATTTCCGAG 1800
Db      1741 AGATGTGTGTGAGGAGGACGCAAGATTTGTGTGATGACCATATGAGAGTGAATTTCCGAG 1800
QY      1801 AGATGTGTGTGAGGAGGATCAATCGTACGATCCAGATCCGATCCGAAAGAAAGTTCCGCG 1860
Db      1801 AGATGTGTGTGAGGAGGATCAATCGTACGATCCAGATCCGATCCGAAAGAAAGTTCCGCG 1860
QY      1861 AGCAGCTAGCTAGGCAATTTGCAATATCTGACCTGTACTGATGATATGCTACGAGATTC 1920
Db      1861 AGCAGCTAGCTAGGCAATTTGCAATATCTGACCTGTACTGATGATATGCTACGAGATTC 1920

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QY      1921 CTAAATGCGCTGTGCATTCACCAACCATCAACGTGAGGAAGGTCATGAGATTCAGCAAG 1980
Db      1921 CTAAATGCGCTGTGCATTCACCAACCATCAACGTGAGGAAGGTCATGAGATTCAGCAAG 1980
QY      1981 CCGCCACCCGAAACCGTCTTTGTGTGAGAGATGAGAGGATGATTCGATCTGCGCCGTTGCA 2040
Db      1981 CCGCCACCCGAAACCGTCTTTGTGTGAGAGATGAGAGGATGATTCGATCTGCGCCGTTGCA 2040
QY      2041 ACATTAAGAAATATTCCTACTCTCATGATGATGATACACCTGCTGTTCTCATGACCGCA 2100
Db      2041 ACATTAAGAAATATTCCTACTCTCATGATGATGATGATACACCTGCTGTTCTCATGACCGCA 2100
QY      2101 GCGCTTAAGTCCCAACATTTTCCAGATGAGAGCTACGCGCGTGCCTATGAGATTCGCTT 2160
Db      2101 GCGCTTAAGTCCCAACATTTTCCAGATGAGAGCTACGCGCGTGCCTATGAGATTCGCTT 2160

RESULT 3
AA165506
ID      AA165506 standard; DNA; 2160 BP.
XX
XX      AA165506:
XX
XX      10-DEC-2001 (first entry)
XX
XX      Nucleotide sequence of the Corynebacterium poxb gene.
XX
XX      gnd gene; 6-phosphogluconate dehydrogenase; L-amino acid; L-lysine;
XX      L-threonine; L-tryptophan; poxb gene; pyruvate oxidase; ss.
XX      Corynebacterium glutamicum.
XX
XX      Key
XX      Location/Qualifiers
XX      CDS
XX      327..2066
XX      /tag= a
XX      /product= "pyruvate oxidase"

W0200171012-A1.
PD      27-SEP-2001.
XX
XX      05-JUL-2000; 2000WD-EP06299.
XX
XX      20-MAR-2000; 2000US-0531265.
XX
XX      (DECS ) DECUSSA AG.
XX      (UNIV NAT IRELAND.
XX
XX      Dunlcau LR, McCormack A, Stapleton C, Burke K, Moeckel B;
XX      WPI; 2001-602792/68.
XX      P-PSDB; AAG79096.
XX
XX      Preparing L-amino acids by fermenting corynebacterium bacteria transformed
XX      with the 6-phosphogluconate dehydrogenase gene is particularly useful
XX      to produce L-lysine and L-threonine
XX
XX      Example 9; Page 47-50; 59pp; English.
XX
XX      The present sequence represents the poxb gene of Corynebacterium
XX      glutamicum. The poxb gene encodes a pyruvate oxidase enzyme. The
XX      poxb gene and the gnd gene are used to produce recombinant bacteria
XX      for use in the course of the invention. The gnd gene encodes a
XX      6-phosphogluconate dehydrogenase enzyme. The specification describes
XX      a method for the fermentative preparation of L-amino acids, in
XX      particular L-lysine, L-threonine, and L-tryptophan. The method comprises
XX      fermenting corynebacterium bacteria in which at least the gnd gene is
XX      amplified and overexpressed. The L-amino acids produced are used in
XX      animal nutrition, human medicine and the pharmaceuticals industry.
XX
XX      Sequence 2160 BP; 491 A; 486 C; 647 G; 536 T; 0 other;

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Query Match		100.0%	Score 2160:	DB 22:	Length 2160:
Best Local Similarity		100.0%	Pred. No. 0:		
Matches 2160:		Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
QY	1	TTAGAGCGATTCTGTGAGGTCTACTTTTGTGGGGTGGGGTCTAAATTTGGCCAGTTT	60		
DB	1	TTAGAGCGATTCTGTGAGGTCTACTTTTGTGGGGTGGGGTCTAAATTTGGCCAGTTT	60		
QY	61	CGAGGCGACGAGAGGGTCCACGATGTTTAAATAGGAGATGGGGATCTGTG	120		
DB	61	CGAGGCGACGAGAGGGTCCACGATGTTTAAATAGGAGATGGGGATCTGTG	120		
QY	121	TTGGTTTCGAGGGCTGAACCAACAGACTGCCAGCAACGAGAAATCCCAAAGT	180		
DB	121	TTGGTTTCGAGGGCTGAACCAACAGACTGCCAGCAACGAGAAATCCCAAAGT	180		
QY	181	GGGATCCCTTTGGTATCCGATACCCACCGGGGCTGAACCTCCCTGGAGGGGGG	240		
DB	181	GGGATCCCTTTGGTATCCGATACCCACCGGGGCTGAACCTCCCTGGAGGGGGG	240		
QY	241	AAGCGTGGCAACACTGGATTTAAGACACATTTGAAGTGCACACAGTTAGGCAAC	300		
DB	241	AAGCGTGGCAACACTGGATTTAAGACACATTTGAAGTGCACACAGTTAGGCAAC	300		
QY	301	AATACCCATTAACGTTGAGAGATTGAGATGACACAGCTAGCAGAACATTAATGACA	360		
DB	301	AATACCCATTAACGTTGAGAGATTGAGATGACACAGCTAGCAGAACATTAATGACA	360		
QY	361	CTTTGGAAGCTCAAGGTGTGAAGCAATTTATGTTTGGTGGTGGAGACGCTTATCCGA	420		
DB	361	CTTTGGAAGCTCAAGGTGTGAAGCAATTTATGTTTGGTGGTGGAGACGCTTATCCGA	420		
QY	421	TCGTGATGCTGTCCGCCAATCAGATATTGAGTGGGTGACGTTTCGAATGAGAGCGG	480		
DB	421	TCGTGATGCTGTCCGCCAATCAGATATTGAGTGGGTGACGTTTCGAATGAGAGCGG	480		
QY	481	CGGCGTTTGCAGCCGGTGGGATGTCATCAGTGGGGAGCTGGCAGTATGCTGCTT	540		
DB	481	CGGCGTTTGCAGCCGGTGGGATGTCATCAGTGGGGAGCTGGCAGTATGCTGCTT	540		
QY	541	CTTGTGCTCTGGAAACACACACTGATTCAGGGCTTTTATGATTGCGATCGAAATGGTG	600		
DB	541	CTTGTGCTCTGGAAACACACACTGATTCAGGGCTTTTATGATTGCGATCGAAATGGTG	600		
QY	601	CGAAGGTGTGGCCATTCCTAGCCATTTCCGAGAGCCAGATGGTTCGACGTTTCC	660		
DB	601	CGAAGGTGTGGCCATTCCTAGCCATTTCCGAGAGCCAGATGGTTCGACGTTTCC	660		
QY	661	AGGAAGCATCCGAGATTTTGTAAAGAAATGCTGTGTTACTGCGAGATGGGAATG	720		
DB	661	AGGAAGCATCCGAGATTTTGTAAAGAAATGCTGTGTTACTGCGAGATGGGAATG	720		
QY	721	GTGGTGGAGAGGGTGAAGCATTTTGCATACGGGATTCAGTCCATGGGGGTAAAG	780		
DB	721	GTGGTGGAGAGGGTGAAGCATTTTGCATACGGGATTCAGTCCATGGGGGTAAAG	780		
QY	781	GTGTGCGGTGTAGTGTCTGTGATATCGCTAAGAGAGAGAGAGAGAGTACGTAAT	840		
DB	781	GTGTGCGGTGTAGTGTCTGTGATATCGCTAAGAGAGAGAGAGAGAGTACGTAAT	840		
QY	841	AFTCCAAATTCACATTTCTCTGCGACTCCTGTGTGTCTCCGGATCTTACTGAAGCTG	900		
DB	841	AFTCCAAATTCACATTTCTCTGCGACTCCTGTGTGTCTCCGGATCTTACTGAAGCTG	900		
QY	901	CAGCGCTGTGGAGCGATTAAACAGCTAAGTGTGATTTGTTGCGGGTGGGGCG	960		
DB	901	CAGCGCTGTGGAGCGATTAAACAGCTAAGTGTGATTTGTTGCGGGTGGGGCG	960		
QY	961	TCAGAAATGCTGCGCGCAGAGTGTGGAGTTGGCGAGAAATTAATCAACCGATCGGGC	1020		
DB	961	TCAGAAATGCTGCGCGCAGAGTGTGGAGTTGGCGAGAAATTAATCAACCGATCGGGC	1020		
QY	1021	ATGCGCTGGTGTGAAGATACATCCAGCATGAGAAATCCGTTGAGGTCCGCAATGCTG	1080		
DB	1021	ATGCGCTGGTGTGAAGATACATCCAGCATGAGAAATCCGTTGAGGTCCGCAATGCTG	1080		
QY	1081	GCCTGCTGTGTTACGGCGCTGCGTGTGATGCGTCCATATAGGGGATCTGTGATCTAT	1140		
DB	1081	GCCTGCTGTGTTACGGCGCTGCGTGTGATGCGTCCATATAGGGGATCTGTGATCTAT	1140		
QY	1141	TGGTACGATTTCCCTTATTCGATTTCTTCTTAAAGCAACAGTTGGCCAGGTGATA	1200		
DB	1141	TGGTACGATTTCCCTTATTCGATTTCTTCTTAAAGCAACAGTTGGCCAGGTGATA	1200		
QY	1201	TCAGGCTGGCACAATTTGTGACGATPACACAGGTGAAGTATCCGCTGACCGGTATG	1260		
DB	1201	TCAGGCTGGCACAATTTGTGACGATPACACAGGTGAAGTATCCGCTGACCGGTATG	1260		
QY	1261	CTGCACAAATCGAAATATTTTCCCTCATGTGAGGAAAAACAGATCGTCTCTCTG	1320		
DB	1261	CTGCACAAATCGAAATATTTTCCCTCATGTGAGGAAAAACAGATCGTCTCTCTG	1320		
QY	1321	ATCGATGCTCAAGGACACAGACGATTAAGTGAAGTGGTGTAGAGACGTACACATA	1380		
DB	1321	ATCGATGCTCAAGGACACAGACGATTAAGTGAAGTGGTGTAGAGACGTACACATA	1380		
QY	1381	ACGTCGAGAGCATGTCCTATTCACCCGTAATACGTTGCTTATTTGAAGAGCTG	1440		
DB	1381	ACGTCGAGAGCATGTCCTATTCACCCGTAATACGTTGCTTATTTGAAGAGCTG	1440		
QY	1441	CGGATTAAGATGCGGTGTTTACTGTGATACCGGCAATGTCAMATGTGTGGCATGCAAGT	1500		
DB	1441	CGGATTAAGATGCGGTGTTTACTGTGATACCGGCAATGTCAMATGTGTGGCATGCAAGT	1500		
QY	1501	ACATCGAATTCGCGAGAGAACCGGACATTTTGGTTCATTTCCGACGACGATG	1560		
DB	1501	ACATCGAATTCGCGAGAGAACCGGACATTTTGGTTCATTTCCGACGACGATG	1560		
QY	1561	CTAATGCTGCTCATGCGATTTGTCGGAAGTGTGTCGAAACCGGACAGTATG	1620		
DB	1561	CTAATGCTGCTCATGCGATTTGTCGGAAGTGTGTCGAAACCGGACAGTATG	1620		
QY	1621	CGATGTGTGCGATGTGTGTTGGGCTGCTGGGTGAGCTTGTACCGTTAAGCTG	1680		
DB	1621	CGATGTGTGCGATGTGTGTTGGGCTGCTGGGTGAGCTTGTACCGTTAAGCTG	1680		
QY	1681	ACCAACTTCGCGGAAGAGCTGTGTGTTTAAACAAGTCTTTGGGACATGTAAGTTG	1740		
DB	1681	ACCAACTTCGCGGAAGAGCTGTGTGTTTAAACAAGTCTTTGGGACATGTAAGTTG	1740		
QY	1741	AGATGCTGTGGAAGGACACGCAATTTGTAAGTACCATGAGAGAGATGATTTGCGAG	1800		
DB	1741	AGATGCTGTGGAAGGACACGCAATTTGTAAGTACCATGAGAGAGATGATTTGCGAG	1800		
QY	1801	AGATTGGGGGCTGGCGGTATCAAAATCGGTACGATCAGCGATCCGAAAGATTCGCG	1860		
DB	1801	AGATTGGGGGCTGGCGGTATCAAAATCGGTACGATCAGCGATCCGAAAGATTCGCG	1860		
QY	1861	AGCAGTAGCTGAGAGCATTTGGCATATCTTGACCTGTACTGATGATATGCTACAGATC	1920		
DB	1861	AGCAGTAGCTGAGAGCATTTGGCATATCTTGACCTGTACTGATGATATGCTACAGATC	1920		
QY	1921	CTAATGCTGTGATCCACCAACATTCACGTGGGAACAGTATGGGATTCAGCAGG	1980		
DB	1921	CTAATGCTGTGATCCACCAACATTCACGTGGGAACAGTATGGGATTCAGCAGG	1980		
QY	1981	CGGCGACCGAAGCGTTTGTGGAGAGATAGAGAGATGATCTGGCGGTTCGA	2040		
DB	1981	CGGCGACCGAAGCGTTTGTGGAGAGATAGAGAGATGATCTGGCGGTTCGA	2040		
QY	2041	ACATTAAGAAATATCTTACTCATGATGATTTATACACTGCTGTCTCATTTGACGCGGA	2100		
DB	2041	ACATTAAGAAATATCTTACTCATGATGATTTATACACTGCTGTCTCATTTGACGCGGA	2100		
QY	2101	GGCGTTAAGTCCCAACATTTCCAGATGGAGCTCAAGCGGGTCCATGATGATGGCTT	2160		
DB	2101	GGCGTTAAGTCCCAACATTTCCAGATGGAGCTCAAGCGGGTCCATGATGATGGCTT	2160		

D	b		1141	TGGGTAGGAAATTCCTCCATTTCGATTTCTCCTCGATAAAGCAACAGTGGCCAGGTGAGTA	1200
Q	y		1201	TCAACGGTGGGCACATTTGCTCGACGTACCAACGGTGGAATACCGGTACCGGTGATCTTG	1260
D	b		1201	TC AACGGTGGCACATTTGGTGGACGTACCACGGGAAGTATCCGGTACCGGTGATCTTG	1260
Q	y		1261	CTCCACAATCGAAAATATTTTGCTCTCATCTGAAAGAAAAACAGATCGTTCCTCTTG	1320
D	b		1261	CTCCACAATCGAAAATATTTTGCTCTCATCTGAAAGAAAAACAGATCGTTCCTCTTG	1320
Q	y		1321	ATCGGATGCTCAAAGCACACGACGCTTAAGTTGAGCTGGTGGTAGAGACTACACACATA	1380
D	b		1321	ATCGGATGCTCAAAGCACACGACGCTTAAGTTGAGCTGGTGGTAGAGACTACACACATA	1380
Q	y		1381	ACGTCGAGAAGCATGTGCTATTACACCTGCAATACGTACGTGCTCATTTTGGACAGCTGG	1440
D	b		1381	ACGTCGAGAAGCATGTGCTATTACACCTGCAATACGTACGTGCTCATTTTGGACAGCTGG	1440
Q	y		1441	CGGATTAAGATCGCGGTGTTTACTGTGTGATACCGGCATGTGCATGTGTGGCATGCGAGT	1500
D	b		1441	CGGATTAAGATCGCGGTGTTTACTGTGTGATACCGGCATGTGCATGTGTGGCATGCGAGT	1500
Q	y		1501	ACATCGAGATCCGAGAGGAACGGGACACTTGTGGGTGTTATTCGCCACGGCCAGATGG	1560
D	b		1501	ACATCGAGATCCGAGAGGAACGGGACACTTGTGGGTGTTATTCGCCACGGCCAGATGG	1560
Q	y		1561	CTAATGCGTTGCCTCATGCGATGEGTGGCAAGTGTGATCGAAACCGCCAGGTGATCG	1620
D	b		1561	CTAATGCGTTGCCTCATGCGATGEGTGGCAAGTGTGATCGAAACCGCCAGGTGATCG	1620
Q	y		1621	CGATGTGTGGCGATNGTGTGTGGGCAATGCGTGGGTGAGCTTCGACGGTTAAGCTGC	1680
D	b		1621	CGATGTGTGGCGATNGTGTGTGGGCAATGCGTGGGTGAGCTTCGACGGTTAAGCTGC	1680
Q	y		1681	ACCAACTTCCGCTGAAGGCTGTGTGTTTAAACAACAGTCTTTTGGGCATGGTGAAGTGG	1740
D	b		1681	ACCAACTTCCGCTGAAGGCTGTGTGTTTAAACAACAGTCTTTTGGGCATGGTGAAGTGG	1740
Q	y		1741	AGATGCTGTGGAGGAGGACGCGAATTTGGTACTGACANTGAGAGATGGAATTTCCAG	1800
D	b		1741	AGATGCTGTGGAGGAGGACGCGAATTTGGTACTGACANTGAGAGATGGAATTTCCAG	1800
Q	y		1801	AGATTTGGGGGGCTGCGGGTATCCAATCGGTACGCATCACCGATCCGANAAGATTTGCG	1860
D	b		1801	AGATTTGGGGGGCTGCGGGTATCCAATCGGTACGCATCACCGATCCGANAAGATTTGCG	1860
Q	y		1861	AGCGATGAGCTGAGGACATTTGGCAATCTGGACCTGATGATGATGATCTGCACGATC	1920
D	b		1861	AGCGATGAGCTGAGGACATTTGGCAATCTGGACCTGATGATGATGATCTGCACGATC	1920
Q	y		1921	CTAATGCGCTGTGCATCCCAACAACCATCAAGTGGGAACAGGTATGGGATTCAGCAAG	1980
D	b		1921	CTAATGCGCTGTGCATCCCAACAACCATCAAGTGGGAACAGGTATGGGATTCAGCAAG	1980
Q	y		1981	CGGCGACCCGACCGCTTTGTGGTGGAGAGAGAGAGATGATGATCTGGCCCGTTTGA	2040
D	b		1981	CGGCGACCCGACCGCTTTGTGGTGGAGAGAGAGAGATGATGATCTGGCCCGTTTGA	2040
Q	y		2041	ACATTAAGGAATATTCTACTACTCATGATGATTTGATACACTGCTTTTCATTTGACCGGA	2100
D	b		2041	ACATTAAGGAATATTCTACTACTCATGATGATTTGATACACTGCTTTTCATTTGACCGGA	2100
Q	y		2101	GCGGTTAACTGCCAACATTTTCACAGATGGGACGTCAACCGGTGGCCATGAGATTTGCCCT	2160
D	b		2101	GCGGTTAACTGCCAACATTTTCACAGATGGGACGTCAACCGGTGGCCATGAGATTTGCCCT	2160

RESULT 5
ABL58754
ID ABL58754 standard; DNA; 2160 BP

AC ABL58754
XX

Query Match	Best Local Similarity	100.0%;	Score 2160;	DB 24;	Length 2160;	
Matches 2160;	Conservative	100.0%;	Pred. No. 0;	Mismatches 0;	Indels 0;	Gaps 0;
0Y	1	TTAGAGCGGATTCCTGTGAGTCACTTTTGTGGGGTCCGGGCTCTAAATTTGGCCAGTTT	60			
Db	1	TTAAGAGCGGATTCCTGTGAGTCACTTTTGTGGGGTCCGGGCTCTAAATTTGGCCAGTTT	60			
0Y	61	CGAGCGCGACAGAGCGGCTGCCACAGATGTTTAAATAGGCGATCGGTGGCATCTGTGT	120			
Db	61	CGAGCGCGACAGAGCGGCTGCCACAGATGTTTAAATAGGCGATCGGTGGCATCTGTGT	120			
0Y	121	TTGGTTTCGACGGGCTGAACCAACAGACTGCCACGACAGAGCGGAAATCCCAAAAGT	180			
Db	121	TTGGTTTCGACGGGCTGAACCAACAGACTGCCACGACAGAGCGGAAATCCCAAAAGT	180			
0Y	181	GGGATCCCTGTTTGGTACCGAGTACCCACCCGGGCGGAAATCCCTGGGAGGGGGCG	240			
Db	181	GGGATCCCTGTTTGGTACCGAGTACCCACCCGGGCGGAAATCCCTGGGAGGGGGCG	240			
0Y	241	AAGCGTGCAACAACCTGGAATTTAAGAGCAGCAATTGAAGTGGACCAAGTAGGCAACAC	300			

Db 241 AAGGTGGCAACACTGGATTTAAAGGCAATTTGAAGTCGACCCAGTAAAGGCAACAC 300
Qy 301 AATAGCCATTAAGCTTGAAGAGTTTCAGATGGCACACAGCTACGAGAACTTAATTGACA 360
Db 301 AATAGCCATTAAGCTTGAAGAGTTTCAGATGGCACACAGCTACGAGAACTTAATTGACA 360
Qy 361 CTTTGAAGCTCAAGGTGTGAAGGAAATTTATGTTGGTGGGTGACAGCTTAATCCGA 420
Db 361 CTTTGAAGCTCAAGGTGTGAAGGAAATTTATGTTGGTGGGTGACAGCTTAATCCGA 420
Qy 421 TCGTGATGCTGTCCGCCAATCAGATATTGATGGGTGGACGTTCCGAATGAGAAAGCGG 480
Db 421 TCGTGATGCTGTCCGCCAATCAGATATTGATGGGTGGACGTTCCGAATGAGAAAGCGG 480
Qy 481 CGGCGTTTGACAGCCGGTGGGGAATCGTGTACTGCTGGGAGCTGGCAGTATGTCTTC 540
Db 481 CGGCGTTTGACAGCCGGTGGGGAATCGTGTACTGCTGGGAGCTGGCAGTATGTCTTC 540
Qy 541 CTTGTGTCCTGGAACACACACCTGATTCAGGGTCTTATGATTCGCATCGAAATGCTG 600
Db 541 CTTGTGTCCTGGAACACACACCTGATTCAGGGTCTTATGATTCGCATCGAAATGCTG 600
Qy 601 CGAAGGTGTTGGCCATCGCTAGCCATATTCAGAGTCCGAGATTGGTTCGACGTTCTCC 660
Db 601 CGAAGGTGTTGGCCATCGCTAGCCATATTCAGAGTCCGAGATTGGTTCGACGTTCTCC 660
Qy 661 AGGAAGCATCGGAGATTTTGTAAAGAAATGCTCTGTACTCGAGATGCTGAATG 720
Db 661 AGGAAGCATCGGAGATTTTGTAAAGAAATGCTCTGTACTCGAGATGCTGAATG 720
Qy 721 GTGTGAGCAGGGTGAACGATTTTGTATCAGCGCGATTCAGTCCACATGAGGGGGTAAAG 780
Db 721 GTGTGAGCAGGGTGAACGATTTTGTATCAGCGCGATTCAGTCCACATGAGGGGGTAAAG 780
Qy 781 GTGTGCGGTGATGATTCCTGTGTATTCGTAAGAGACGAGGTGACGTAATCT 840
Db 781 GTGTGCGGTGATGATTCCTGTGTATTCGTAAGAGACGAGGTGACGTAATCT 840
Qy 841 ATTCCAATTCACACTATTTCTGTGACACCTGCTGTGTCTCCGAGTCTACTGAGCGTG 900
Db 841 ATTCCAATTCACACTATTTCTGTGACACCTGCTGTGTCTCCGAGTCTACTGAGCGTG 900
Qy 901 CAGCGGTGTGAGGCGATTAAACAACGCTAGTCTGTCTCTGTCGCGGGCGGGG 960
Db 901 CAGCGGTGTGAGGCGATTAAACAACGCTAGTCTGTCTCTGTCGCGGGCGGGG 960
Qy 961 TGAAGAATGCTCGCGCGAGGTGTGAGATTGCGGAGAAAGATTAAATCACGATCGGGC 1020
Db 961 TGAAGAATGCTCGCGCGAGGTGTGAGATTGCGGAGAAAGATTAAATCACGATCGGGC 1020
Qy 1021 ATGCGCTGGGTGATGAGCAGTACATCCAGCATGAGAAATCCGTTTGAAGGTCCGATGCTG 1080
Db 1021 ATGCGCTGGGTGATGAGCAGTACATCCAGCATGAGAAATCCGTTTGAAGGTCCGATGCTG 1080
Qy 1081 GCCTCTGTTGTTAGCGCGCTGCTGTGATCGCTCCAAATGAGCGGATCTGATTTCTAT 1140
Db 1081 GCCTCTGTTGTTAGCGCGCTGCTGTGATCGCTCCAAATGAGCGGATCTGATTTCTAT 1140
Qy 1141 TGGGTAGGATTTCCCTATTCGTATTCCTTCTTAAGACACAGTTGCCAGGTGATTA 1200
Db 1141 TGGGTAGGATTTCCCTATTCGTATTCCTTCTTAAGACACAGTTGCCAGGTGATTA 1200
Qy 1201 TCAAGGTGCGCACATTGTCGACGTACACAGGTTAAGTATCCGTTGACCGGTGATGTTG 1260
Db 1201 TCAAGGTGCGCACATTGTCGACGTACACAGGTTAAGTATCCGTTGACCGGTGATGTTG 1260
Qy 1261 CTGCAACATCGAAAAATTTTGTCTCATGTGAAGAAAAAACAAGATGTTCTCTCTTG 1320
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Qy 1321 ATCGATGCTCAAGGCAAGAGGTAGTGTGAGTCCGTGTGAGACGTACACACATA 1380
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Db 1321 ATCGATGCTCAAGGCAAGAGGTAGTGTGAGTCCGTGTGAGACGTACACACATA 1380
Qy 1381 ACGTCGAGAACATGTGCTATTACCCCTGATACGTTGGCTCTATTTTGACAGCTGG 1440
Db 1381 ACGTCGAGAACATGTGCTATTACCCCTGATACGTTGGCTCTATTTTGACAGCTGG 1440
Qy 1441 CGGATTAAGGATGCGGGTGTACTGTGTGATACCGCATGTGCAATGTGTGCGATCGAGT 1500
Db 1441 CGGATTAAGGATGCGGGTGTACTGTGTGATACCGCATGTGCAATGTGTGCGATCGAGT 1500
Qy 1501 ACATCGAAGATCCGAGAGGAACCGCGCATTTGTGGGTTCAATCCGCCACGCGACATGG 1560
Db 1501 ACATCGAAGATCCGAGAGGAACCGCGCATTTGTGGGTTCAATCCGCCACGCGACATGG 1560
Qy 1561 CTATATGCTGGCCATGACGATTTGTGTCGGAAGATGTGATCCGAACCCGAGTGTATG 1620
Db 1561 CTATATGCTGGCCATGACGATTTGTGTCGGAAGATGTGATCCGAACCCGAGTGTATG 1620
Qy 1621 CGATGTGTGCGATGTGTGTTGGGATGCTGTGCGGTGAGACTTCTGACGTTAAAGCTGC 1680
Db 1621 CGATGTGTGCGATGTGTGTTGGGATGCTGTGCGGTGAGACTTCTGACGTTAAAGCTGC 1680
Qy 1681 ACCAATCTCCGTGAAGAGCTGTGTGTTTAAACAAGTCTTTTGGCATGAGTAAATGG 1740
Db 1681 ACCAATCTCCGTGAAGAGCTGTGTGTTTAAACAAGTCTTTTGGCATGAGTAAATGG 1740
Qy 1741 AGATGCTGCTGGAAGGACACCCAGAAATTTGTACTGACCATGAGAGAAATTTTCGAC 1800
Db 1741 AGATGCTGCTGGAAGGACACCCAGAAATTTGTACTGACCATGAGAGAAATTTTCGAC 1800
Qy 1801 AGATGCGCGGCTGCGGGGTATCAATGCGTACGATCACCAGTCCGAAGAAAGTTGCG 1860
Db 1801 AGATGCGCGGCTGCGGGGTATCAATGCGTACGATCACCAGTCCGAAGAAAGTTGCG 1860
Qy 1861 AGCAGCTAGCTGAGGATTTGGCATATCTGAGCTGATGATGATGATGATGATGATG 1920
Db 1861 AGCAGCTAGCTGAGGATTTGGCATATCTGAGCTGATGATGATGATGATGATGATG 1920
Qy 1921 CTATATGCTGCTGATCCCAACCAACATCATGCTGAGGAAAGTATGAGTATGAGTATG 1980
Db 1921 CTATATGCTGCTGATCCCAACCAACATCATGCTGAGGAAAGTATGAGTATGAGTATG 1980
Qy 1981 CGGCGCACCGGAACCGCTTTTGGTGAAGAGTGAAGCGATGATGATGATGATGATG 2040
Db 1981 CGGCGCACCGGAACCGCTTTTGGTGAAGAGTGAAGCGATGATGATGATGATGATG 2040
Qy 2041 ACATAGGATATTTCTTACCTCATGATGATGATGATGATGATGATGATGATGATG 2100
Db 2041 ACATAGGATATTTCTTACTCATGATGATGATGATGATGATGATGATGATGATG 2100
Qy 2101 GCGCTTAAGTCCCAACATTTCCAGATGAGTCAAGCGCGGTGCCCATGAGTATGCTCT 2160
Db 2101 GCGCTTAAGTCCCAACATTTCCAGATGAGTCAAGCGCGGTGCCCATGAGTATGCTCT 2160

RESULT 6
ABLS8756
ID ABL8756 standard; DNA; 3248 bp.
XX
AC ABL8756;
XX
DT 05-JUL-2002 (first entry)
XX
DE Corynebacterium poxb encoding polynucleotide seq ID NO 4.
XX
KW Corynebacterium; poxb; pyruvate oxidase; enzyme; fermentative production;
KW D-pantothenic acid; vitamin; medicine; pharmaceutical; food industry;
KW animal nutrition; gene; ds.
XX
OS Corynebacterium glutamicum.
XX
FH Key
CDS Location/Qualifiers
802..2541

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FT      /*tag= c
FT      /product= "poxb"
FT      /EC_number= "1.2.2.2"
XX
XX
XX      DE10117085-A1.
XX
XX      11-APR-2002.
XX
XX      06-APR-2001; 2001DE-1017085.
XX
XX      30-SEP-2000; 2000DE-1048604.
XX
XX      (DEGS ) DESUSSA AG.
XX
XX      Dusch N, Herrmann T, Thierbach G;
XX
XX      WPI: 2002-363950/40.
XX      P-PSDB: ABB79447.
XX
XX      Fermentative production of D-pantothenic acid (I), useful e.g. in
XX      animal nutrition, from coryneform bacteria with reduced activity of the
XX      pyruvate oxidase gene -
XX
XX      Example 4; Page 16-20; 28pp; German.
XX
XX      The invention relates to the fermentative production of D-pantothenic
XX      acid (I) by growing a (I)-producing coryneform bacterium in which the
XX      activity of at least the sequence poxb (AB158754, AB158756) encoding
XX      pyruvate oxidase (AB158755, EC 1.2.2.2) has been weakened, especially
XX      switched off. (I) is then recovered from medium or cells. (I) is a
XX      vitamin useful in human medicine, the pharmaceutical and food industries
XX      and particularly in animal nutrition. Reducing the activity of poxb
XX      improves fermentative production of (I).
XX
XX      Sequence 3248 BP; 744 A; 743 C; 985 G; 776 T; 0 other;
XX
XX      Query Match      100.0%; Score 2160; DB 24; Length 3248;
XX      Best Local Similarity 100.0%; Pred. No. 0;
XX      Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1 TTAAGGCGATTCTGTGAGTCACTTTTGTGGGCTCGGGCTCTAAATTTGGCCAGTTT 60
XX      DB      1 TTAAGGCGATTCTGTGAGTCACTTTTGTGGGCTCGGGCTCTAAATTTGGCCAGTTT 535
XX
XX      QY      61 CGAGGCGACGACGAGCGGTGCCCGCATGTTAAATPAGSGATCGGGCATCTGT 120
XX      DB      61 CGAGGCGACGACGAGCGGTGCCCGCATGTTAAATPAGSGATCGGGCATCTGT 595
XX
XX      QY      121 TTGGTTTCGAGCGGGCTGAACCAACGACGACTGCCAGCAAGCAAGCAATCCCAAAAGT 180
XX      DB      121 TTGGTTTCGAGCGGGCTGAACCAACGACGACTGCCAGCAAGCAAGCAATCCCAAAAGT 655
XX
XX      QY      181 GGGCATCCCTGTTGGTACGAGTACCCACCCGGGCTGAACCTCCTGGCAGGCGGGCG 240
XX      DB      181 GGGCATCCCTGTTGGTACGAGTACCCACCCGGGCTGAACCTCCTGGCAGGCGGGCG 715
XX
XX      QY      241 AAGGTGGCAACAACACTGGAATTTAGAGCAATTTAGTGCGCAAGTAAAGTAAAGCAAC 300
XX      DB      241 AAGGTGGCAACAACACTGGAATTTAGAGCAATTTAGTGCGCAAGTAAAGTAAAGCAAC 775
XX
XX      QY      301 AATAGCATATAAGTTGAGAGTTGAGTGCACACACACTACGCGAAGCAATTAATTGACA 360
XX      DB      301 AATAGCATATAAGTTGAGAGTTGAGTGCACACACACTACGCGAAGCAATTAATTGACA 835
XX
XX      QY      361 CTTTGAAGCTCAAGGTGTAAGCGAATTTATGTTGTGGGTGACAGCCTTAATCCGA 420
XX      DB      361 CTTTGAAGCTCAAGGTGTAAGCGAATTTATGTTGTGGGTGACAGCCTTAATCCGA 895
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XX      QY      421 TCGTGATGCTGCCGCAATCAGATATTGATGGGTGCGAGTTGCAAAATGAGAGACGG 480
XX      DB      421 TCGTGATGCTGCCGCAATCAGATATTGATGGGTGCGAGTTGCAAAATGAGAGACGG 955
XX
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DB      956 CGGCGTTTGAGCGCGGTGCGGAATCGTTGATCACTGGGAGCTGGCAGTATGTCGCTT 1015
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XX      DB      1016 CTTGTGCTCTGGAACACACACACTTATAGGGCTCTTTATGATTCGATCGAAATGCTG 1075
XX
XX      QY      601 CGAAGGTGTGGCATCGTAGCATATTCGAGTCCGACGATTTGGTTCACGCTTTC 660
XX      DB      1076 CGAAGGTGTGGCATCGTAGCATATTCGAGTCCGACGATTTGGTTCACGCTTTC 1135
XX
XX      QY      661 AGGAAAGCATCCGCGAGATTTTGTTAAGGAATGCTGTGTTACTGCGAGATGTAATG 720
XX      DB      1136 AGGAAAGCATCCGCGAGATTTTGTTAAGGAATGCTGTGTTACTGCGAGATGTAATG 1195
XX
XX      QY      721 GTGGTAGAGGAGGTGTAACCATTTTTCATTCACCGGATTAAGTCCACCATGCGGTAAG 780
XX      DB      1196 GTGGTAGAGGAGGTGTAACCATTTTTCATTCACCGGATTAAGTCCACCATGCGGTAAG 1255
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XX      QY      781 GTGTGCGGTGATGATTCCTGATATGCGTAAAGCAAGCAGGAGGAGGATCTT 840
XX      DB      1256 GTGTGCGGTGATGATTCCTGATATGCGTAAAGCAAGCAGGAGGAGGATCTT 1315
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XX      DB      1316 ATTCGAATTCACATATTCTCTGCGACTCGTGTGTTCCCGGATCCTACTAGAGCTG 1375
XX
XX      QY      901 CAGCGCTGTGAGGCGATTAACACGCTAAGTCTGCTACTTTGTTCTGCGGTGCGGCG 960
XX      DB      1376 CAGCGCTGTGAGGCGATTAACACGCTAAGTCTGCTACTTTGTTCTGCGGTGCGGCG 1435
XX
XX      QY      961 TGAAGAACTTCGCGCGCAGTGTGAGTGTGGGAGAGAAATTAATACCGATGGGG 1020
XX      DB      1436 TGAAGAACTTCGCGCGCAGTGTGAGTGTGGGAGAGAAATTAATACCGATGGGG 1495
XX
XX      QY      1021 ATGCGCTGCTGTGTAACAGATATCCAGATGAGAATCCGTTTGAAGTGGCGATCTG 1080
XX      DB      1496 ATGCGCTGCTGTGTAACAGATATCCAGATGAGAATCCGTTTGAAGTGGCGATCTG 1555
XX
XX      QY      1081 GCGTCTGTGTTACGCGCGCTCGTGAGTGGTCCAAATGAGCGGATTCGTGATCTAT 1140
XX      DB      1556 GCGTCTGTGTTACGCGCGCTCGTGAGTGGTCCAAATGAGCGGATTCGTGATCTAT 1615
XX
XX      QY      1141 TGGTAGAGATTTCCCTTATTCGTATTCCTTCTTAAGACAAAGCTTGGCCAGTGGATA 1200
XX      DB      1616 TGGTAGAGATTTCCCTTATTCGTATTCCTTCTTAAGACAAAGCTTGGCCAGTGGATA 1675
XX
XX      QY      1201 TCAAGGTGCCACATTTGTGACGTACCCAGGTGAAGTATCCGTTGACCGGTGATGTTG 1260
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XX      QY      1381 ACGTGAAGCAATGTGCTATTGACCTGTAATACGTTGCTCTATTTTGAACGAGCTGG 1440
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XX      QY      1441 CGGATTAAGGATGCGGTGTTTACTGTGATACCGGATGTAAGTGTGGGATGGAGGT 1500
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XX      DB      1976 ACATCGAATCGGAGGAAACGCGCATTTTGTGGTTCAATTCGCGACGCGACGATGG 2035
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XX      QY      1561 CTATGCTGTCCTCAATGCGATGTGTCCGCAAAATGTTGATCGAAACCGCAGGTATCG 1620

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PR 03-SEP-1999; 99DE-1042079.
 PR 03-SEP-1999; 99DE-1042086.
 PR 03-SEP-1999; 99DE-1042087.
 PR 03-SEP-1999; 99DE-1042088.
 PR 03-SEP-1999; 99DE-1042095.
 PR 03-SEP-1999; 99DE-1042123.
 PR 03-SEP-1999; 99DE-1042125.
 XX
 PA (BADI) BASF AG.
 PI Pompejus M, Kroegeer B, Schroeder H, Zelder O, Haberhauer G;
 XX WPI; 2001-061975/07.
 DR P-PSDB; AAB79285.
 XX
 PT New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
 PT metabolism and oxidative phosphorylation protein for production or
 PT modulation of production of fine chemicals e.g. amino acids,
 PT carbohydrates or enzymes -
 XX
 PS Claim 3; Page 268-270; 1246pp; English.
 XX
 CC AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
 CC metabolism and oxidative phosphorylation (SMP) proteins given in
 CC AAB79243 to AAB 79633 which are involved in carbon metabolism and
 CC energy production. The C. glutamicum SMP gene can be used in vectors
 CC (II) for expression in host cells and production or modulation of
 CC production of fine chemicals, such as, an organic acid, a proteogenic
 CC or nonproteogenic amino acid (preferred), a purine or pyrimidine base,
 CC a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty
 CC acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a
 CC cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins
 CC (III) encoded by them are used for diagnosing the presence or activity of
 CC Corynebacterium diptheriae in a subject. (I), (II), (III) or host cells
 CC containing them are used to map genomes of organisms related to
 CC C. glutamicum, identify and localise C. glutamicum sequences of interest,
 CC in evolutionary studies, in determining SMP protein regions required
 CC for function, in modulating SMP protein activity, in modulating the
 CC metabolism of sugars, and in modulating high-energy molecule production
 CC in a cell (i.e. ATP, NADPH).
 CC
 XX
 SO Sequence 1860 BP; 426 A; 405 C; 562 G; 467 T; 0 other;
 Query Match 86.1%; Score 1860; DB 22; Length 1860;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1860; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 421 TTGACGCTTCTTCAGGAAACGCATCCGAGATTTTGAAGAAATGCTGTGTTACTG 480
 QY 707 CGAGATGCTGAATGTGTGTGAGCAGGGTGAACGCATTTTGCATACCCGATTCAGTCAC 766
 Db 481 CGAGATGCTGAATGTGTGTGAGCAGGGTGAACGCATTTTGCATACCCGATTCAGTCAC 540
 QY 767 CATGCGGGGTAAAGGTGTGTCGGTAGTAGATTCGCGATATCCGTAAAGAAAGCC 826
 Db 541 CATGCGGGGTAAAGGTGTGTCGGTAGTAGATTCGCGATATCCGTAAAGAAAGCC 600
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 Db 601 AGGTGACGTAATTTATTCATTTCCATTTCTTCGACATCTGTGTGTCCCGGA 660
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 Db 661 TCCTACTGAGGCTGACGCGCTGTGTGAGGCGATTAACACGCTAAGTCTGACTTGGT 720
 QY 947 CTCGGTGGCGGGGTGAAGATGCTGCGCGCAAGTGTGGAGTGGCGGAGATTTAA 1006
 Db 721 CTCGGTGGCGGGGTGAAGATGCTGCGCGCAAGTGTGGAGTGGCGGAGATTTAA 780
 QY 1007 ATCACCAGATGGGCGATGCGCTGGGTGTGAAGCAGTACATCAGCATGAGATCCGTTGA 1066
 Db 781 ATCACCAGATGGGCGATGCGCTGGGTGTGAAGCAGTACATCAGCATGAGATCCGTTGA 840
 QY 1067 GGTGCGGATGTCGCGCTGCTGTTGACGCGCTGCGTGAGATGCTCAATGAGCGGA 1126
 Db 841 GGTGCGGATGTCGCGCTGCTGTTGACGCGCTGCGTGAGATGCTCAATGAGCGGA 900
 QY 1127 TCGTGATTCCTATTGGGTGCGGATTCCTGTTTCGATTCCTGCTTAAGCAACGT 1186
 Db 901 TCGTGATTCCTATTGGGTGCGGATTCCTGTTTCGATTCCTGCTTAAGCAACGT 960
 QY 1187 TGCCAGGTGTGATATACGCGTGCACATTTGGTCGACGTACACGAGTGAAGTATCCGT 1246
 Db 961 TGCCAGGTGTGATATACGCGTGCACATTTGGTCGACGTACACGAGTGAAGTATCCGT 1200
 QY 1247 GACCGGTGATGTTGCTGCAACATTCGAAATATTTTGGCTCATGTGAAGAAACACA 1306
 Db 1021 GACCGGTGATGTTGCTGCAACATTCGAAATATTTTGGCTCATGTGAAGAAACACA 1080
 QY 1307 TCGTTCCTTCCTTGATGCGATGCTCAAGGCACAGCGCTGAAGTGAAGCTCGGTGTAGA 1366
 Db 1081 TCGTTCCTTCCTTGATGCGATGCTCAAGGCACAGCGCTGAAGTGAAGCTCGGTGTAGA 1140
 QY 1367 GACGTACACATTAACGTGAGAGCATGTGCTATTACACCTGAATACGTTGCTCTAT 1426
 Db 1141 GACGTACACATTAACGTGAGAGCATGTGCTATTACACCTGAATACGTTGCTCTAT 1200
 QY 1427 TTTGAACGAGCTGGCGGATTAAGATGCGGTGTTACTGTGGAATACCGGATGTGCAATGT 1486
 Db 1201 TTTGAACGAGCTGGCGGATTAAGATGCGGTGTTACTGTGGAATACCGGATGTGCAATGT 1260
 QY 1487 GTGCGATGCGAGGTACATGAGAAATCCGAGGGAACGCGCATTTGTGGTTCAATCCG 1546
 Db 1261 GTGCGATGCGAGGTACATGAGAAATCCGAGGGAACGCGCATTTGTGGTTCAATCCG 1320
 QY 1547 CCACGGCACAGATGCGTAATGCTTGCTCATGCGATTTGTTGCGCAAAAGTGTGATCGAAA 1606
 Db 1321 CCACGGCACAGATGCGTAATGCTTGCTCATGCGATTTGTTGCGCAAAAGTGTGATCGAAA 1380
 QY 1607 CCGCAGGTGATCGGATGTGTGCGAGATGCGTGTGGCAATGCTGTGGGAGACTTCT 1666
 Db 1381 CCGCAGGTGATCGGATGTGTGCGAGATGCGTGTGGCAATGCTGTGGGAGACTTCT 1440
 QY 1667 GACCGTTAAGCTGACCAACTTCGCTGAAGGCTGTGTTTAACCAACAGTCTTTGGG 1726
 Db 1441 GACCGTTAAGCTGACCAACTTCGCTGAAGGCTGTGTTTAACCAACAGTCTTTGGG 1500

QY 1727 CATGSGAAGTTGGAGATGCTGCTGGAGGACAGCCAGATTGGTACTGACCATGAGCA 1786
 |||||||
 Db 1501 CATGSGAAGTTGGAGATGCTGCTGGAGGACAGCCAGATTGGTACTGACCATGAGCA 1560
 QY 1787 AGTGAATTTGCGAGATTTGGCGGCTGCGGGGTATCAAAATCGGTACGATCAGCAGATCC 1846
 |||||||
 Db 1561 AGTGAATTTGCGAGATTTGGCGGCTGCGGGGTATCAAAATCGGTACGATCAGCAGATCC 1620
 QY 1847 GAGAAAGTTGGCGAGGAGCTAGCTGAGGACATGGCATATCTGAGACTGTACTGATGCA 1906
 |||||||
 Db 1621 GAGAAAGTTGGCGAGGAGCTAGCTGAGGACATGGCATATCTGAGACTGTACTGATGCA 1680
 QY 1907 TATGCTCAGGATGCTTAATGCGCTGATCCACCAACCATCACTGAGGAAACAGGTGAT 1966
 |||||||
 Db 1681 TATGCTCAGGATGCTTAATGCGCTGATCCACCAACCATCACTGAGGAAACAGGTGAT 1740
 QY 1967 GGGATTTGAGCAAGCGGCGACCCGACCGTCTTTGGTGGAGAGTAGAGGCGATGATGCA 2026
 |||||||
 Db 1741 GGGATTTGAGCAAGCGGCGACCCGACCGTCTTTGGTGGAGAGTAGAGGCGATGATGCA 1800
 QY 2027 TCTGGCCCGTTGAGCATAGGATATCTCTACTCATGATGATGATGATGATGATGATGAT 2086
 |||||||
 Db 1801 TCTGGCCCGTTGAGCATAGGATATCTCTACTCATGATGATGATGATGATGATGATGAT 1860
 RESULT 9
 AAH67838
 ID AAH67838 standard: DNA: 1737 BP.
 XX AAH67838;
 AC
 XX 26-SEP-2001 (first entry)
 DT
 XX
 DE C glutamicum coding sequence fragment SEQ ID NO: 2873.
 XX
 KW Corynebacterium; amino acid synthesis; vitamin; saccharide;
 KM organic acid synthesis; ds.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN EPI108790-A2.
 PD 20-JUN-2001.
 XX
 PE 18-DEC-2000: 2000EP-0127688.
 XX
 PR 16-DEC-1999: 99JP-0377484.
 PR 07-APR-2000: 2000JP-0159162.
 PR 03-AUG-2000: 2000JP-0280988.
 XX
 PA (KYO) KYOWA HAKKO KOGYO KK.
 PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
 PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
 DR WPI: 2001-376931/40.
 DR P-PDB: AAG92619.
 XX
 PT Novel polynucleotides derived from Corynebacterium, for identifying
 PT mutation point of a gene, measuring expression of a gene, analysing
 PT expression profile or pattern of a gene and identifying homologous gene
 PT
 PS Claim 8: SEQ ID NO: 2873; 246pp + Sequence Listing: English.
 XX
 CC The present invention provides a number of nucleotide and protein
 CC sequences from the Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of Corynebacterium glutamicum, measuring expression amount and
 CC analysing the expression profile or expression pattern of a gene derived
 CC from Corynebacterium glutamicum, and identifying a homologous of a gene derived
 CC from Corynebacterium glutamicum. Corynebacterium glutamicum are useful for producing

CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a nucleic acid described
 CC in the exemplification of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC European Patent Office.
 XX
 SO Sequence 1737 BP: 388 A; 380 C; 528 G; 441 T; 0 other;
 Query Match 80.4%; Score 1737; DB 22; Length 1737;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1737; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 327 ATGCGACACGCTGCGAGAAATTAATGACACTTGGAGCTCAAGGTGGAGACCA 386
 |||||||
 Db 1 ATGCGACACGCTGCGAGAAATTAATGACACTTGGAGCTCAAGGTGGAGACCA 60
 QY 387 ATTTATGTTGGTGGGTGACAGGCTTAATCCATGCTGATGCTGCCCAATCAGAT 446
 |||||||
 Db 61 ATTTATGTTGGTGGGTGACAGGCTTAATCCATGCTGATGCTGCCCAATCAGAT 120
 QY 447 ATTAGAGTGGTGGACGCTTCCGAATGAGAGAGGCGGCGTTTGCAGCGGTTGGGATGCG 506
 |||||||
 Db 121 ATTAGAGTGGTGGACGCTTCCGAATGAGAGAGGCGGCGTTTGCAGCGGTTGGGATGCG 180
 QY 507 TTGATCACTGGGAGCTGGCAGATATGCTGCTCTTGTGGTCTGGAACACACACTG 566
 |||||||
 Db 181 TTGATCACTGGGAGCTGGCAGATATGCTGCTCTTGTGGTCTGGAACACACACTG 240
 QY 567 ATTCAGGCTCTTATGATTCGATCGCAAAATGCTGCGAAGGTGTTGGCCATCGTACCAT 626
 |||||||
 Db 241 ATTCAGGCTCTTATGATTCGATCGCAAAATGCTGCGAAGGTGTTGGCCATCGTACCAT 300
 QY 627 ATTCGAGTGGCCGATGTTGTTGACGCTTCTCCAGAAACGATCCGAGATTTGTT 686
 |||||||
 Db 301 ATTCGAGTGGCCGATGTTGTTGACGCTTCTCCAGAAACGATCCGAGATTTGTT 360
 QY 687 AAGGAATGCTGTGTTACTGCGAGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 746
 |||||||
 Db 361 AAGGAATGCTGTGTTACTGCGAGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 420
 QY 747 CATCAGCGGATTCAGTCCACCATGCGGCGGTAAGAGTGTGCGTGAAGATTCGCGT 806
 |||||||
 Db 421 CATCAGCGGATTCAGTCCACCATGCGGCGGTAAGAGTGTGCGTGAAGATTCGCGT 480
 QY 807 GATATCGCTAAGAAAGCAGGATGACGATCTTATTCGAATTCACATTTCTTCTGCG 866
 |||||||
 Db 481 GATATCGCTAAGAAAGCAGGATGACGATCTTATTCGAATTCACATTTCTTCTGCG 540
 QY 867 ACTCCTGTTGTTCCCGGATCCGATGAGGCTGCGAGCGGTTGGAGGCGATTAACAC 926
 |||||||
 Db 541 ACTCCTGTTGTTCCCGGATCCGATGAGGCTGCGAGCGGTTGGAGGCGATTAACAC 600
 QY 927 GCTAAGTCTGCTACCTTGTCTTCCGCGTGGCGGCTGAAGATGCTCCGCGCAGCTGTG 986
 |||||||
 Db 601 GCTAAGTCTGCTACCTTGTCTTCCGCGTGGCGGCTGAAGATGCTCCGCGCAGCTGTG 660
 QY 987 GAGTTGGCGGAGATTAATTAACCGATGCGGATCGCTGGTGGTGAACAGTACATC 1046
 |||||||
 Db 661 GAGTTGGCGGAGATTAATTAACCGATGCGGATCGCTGGTGGTGAACAGTACATC 720
 QY 1047 CAGATGAGATTCGTTGAGTGGGATGCTGCGGCTGCTGTTGAGGCGGCTGCGTG 1106
 |||||||
 Db 721 CAGATGAGATTCGTTGAGTGGGATGCTGCGGCTGCTGTTGAGGCGGCTGCGTG 780
 QY 1107 GATGCTGCAATGAGCGGATCTCTGATTTATTTGGTACGATTTCCCTTATTCGAT 1166
 |||||||
 Db 781 GATGCTGCAATGAGCGGATCTCTGATTTATTTGGTACGATTTCCCTTATTCGAT 840
 QY 1167 TTCTTCTTAAGCAACGTTGCCAGTGGATATCAAGGTTGGCATTTGGTGGAGCT 1226
 |||||||
 Db 841 TTCTTCTTAAGCAACGTTGCCAGTGGATATCAAGGTTGGCATTTGGTGGAGCT 900

QY 1227 ACCACGGTGAATATCCGGTACCGGATGATGTTGTCACAAATCGAAAATATTTGGCT 1286
 |||||||
 DB 901 ACCACGGTGAATATCCGGTACCGGATGATGTTGTCACAAATCGAAAATATTTGGCT 960
 |||||||
 QY 1287 CATGTGAAGAAAAAACAAGATCGTCTTCTTCCTTGATGGATGCTCAGCAGCAGCGT 1346
 |||||||
 DB 961 CATGTGAAGAAAAAACAAGATCGTCTTCTTCCTTGATGGATGCTCAGCAGCAGCGT 1020
 |||||||
 QY 1347 AAGTTGAGCTCGGTGAGAGAGTACACATACGTCAGAGATGAGCTATTCAC 1406
 |||||||
 DB 1021 AAGTTGAGCTCGGTGAGAGAGTACACATACGTCAGAGATGAGCTATTCAC 1080
 |||||||
 QY 1407 CCTGAATACGTTGCTCTATTTTGAACGAGCTGGCGAATTAAGATGCGGTATTACTG 1466
 |||||||
 DB 1081 CCTGAATACGTTGCTCTATTTTGAACGAGCTGGCGAATTAAGATGCGGTATTACTG 1140
 |||||||
 QY 1467 GATACGGGATGAGATGATGTCGAGAGAGGATGATGATGATGATGATGATGATGATG 1526
 |||||||
 DB 1141 GATACGGGATGAGATGATGTCGAGAGAGGATGATGATGATGATGATGATGATGATG 1200
 |||||||
 QY 1527 GACTTTGAGTTCATTCGCCACAGGAGATGCTAATGCTTGCCTCATGCGATTGAT 1586
 |||||||
 DB 1201 GACTTTGAGTTCATTCGCCACAGGAGATGCTAATGCTTGCCTCATGCGATTGAT 1260
 |||||||
 QY 1587 GCGCAAGTGTGATGCAAAACCCGACAGATGCGATGCGATGCGATGCGATGCGATG 1646
 |||||||
 DB 1261 GCGCAAGTGTGATGCAAAACCCGACAGATGCGATGCGATGCGATGCGATGCGATG 1320
 |||||||
 QY 1647 ATGCTGCTGGTGAAGCTTTCGACCGCTTAACCTCAGCCACTTCGCTGAAGGCTGTG 1706
 |||||||
 DB 1321 ATGCTGCTGGTGAAGCTTTCGACCGCTTAACCTCAGCCACTTCGCTGAAGGCTGTG 1380
 |||||||
 QY 1707 TTTTAAACAAGTCTTGGGCGATGAGATGAGATGCTCTGAGAGGACAGCCAGAA 1766
 |||||||
 DB 1381 TTTTAAACAAGTCTTGGGCGATGAGATGAGATGCTCTGAGAGGACAGCCAGAA 1440
 |||||||
 QY 1767 TTTGCTAGTACCATGAGAGATGATTTGTCAGAGATTTGCGGCGCTGCGGCTATCAA 1826
 |||||||
 DB 1441 TTTGCTAGTACCATGAGAGATGATTTGTCAGAGATTTGCGGCGCTGCGGCTATCAA 1500
 |||||||
 QY 1827 TCGGTACGATCACCAGTCCGAGAAAGTTCGCGAGAGTACTGAGGATTTGGCATAT 1886
 |||||||
 DB 1501 TCGGTACGATCACCAGTCCGAGAAAGTTCGCGAGAGTACTGAGGATTTGGCATAT 1560
 |||||||
 QY 1887 CCTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1946
 |||||||
 DB 1561 CCTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
 |||||||
 QY 1947 ATCAGCTGGAGAACGATGATGATGATGATGATGATGATGATGATGATGATGATG 2006
 |||||||
 DB 1621 ATCAGCTGGAGAACGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
 |||||||
 QY 2007 GGAAGTAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2063
 |||||||
 DB 1681 GGAAGTAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1737
 |||||||
 RESULT 10
 AAF71404
 ID AAF71404 standard; DNA; 944 BP.
 XX AAF71404:
 AC 30-APR-2001 (first entry)
 DE Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO: 89.
 XX
 XX
 DE Corynebacterium glutamicum; carbon metabolism and oxidative phosphorylation protein;
 KW SMP protein; sugar metabolism and oxidative phosphorylation protein;
 KW fine chemical production; organic acid; proteinogenic amino acid;
 KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
 KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
 KW carbohydrate; aromatic compound; vitamin; cofactor; polypeptide; enzyme;

KW diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN W0200100844-A2.
 PD 04-JAN-2001.
 PF 23-JUN-2000; 2000MO-1B00943.
 PR 25-JUN-1999; 99US-0141031.
 PR 08-JUL-1999; 99DE-1031412.
 PR 08-JUL-1999; 99DE-1031413.
 PR 08-JUL-1999; 99DE-1031419.
 PR 08-JUL-1999; 99DE-1031420.
 PR 08-JUL-1999; 99DE-1031424.
 PR 08-JUL-1999; 99DE-1031428.
 PR 08-JUL-1999; 99DE-1031431.
 PR 08-JUL-1999; 99DE-1031434.
 PR 08-JUL-1999; 99DE-1031510.
 PR 08-JUL-1999; 99DE-1031562.
 PR 08-JUL-1999; 99DE-1031634.
 PR 09-JUL-1999; 99DE-1032180.
 PR 09-JUL-1999; 99DE-1032227.
 PR 09-JUL-1999; 99DE-1032230.
 PR 09-JUL-1999; 99US-0143208.
 PR 14-JUL-1999; 99DE-1032924.
 PR 14-JUL-1999; 99DE-1032973.
 PR 14-JUL-1999; 99DE-1033005.
 PR 27-AUG-1999; 99DE-1040765.
 PR 31-AUG-1999; 99US-0151572.
 PR 03-SEP-1999; 99DE-1042076.
 PR 03-SEP-1999; 99DE-1042079.
 PR 03-SEP-1999; 99DE-1042086.
 PR 03-SEP-1999; 99DE-1042087.
 PR 03-SEP-1999; 99DE-1042088.
 PR 03-SEP-1999; 99DE-1042095.
 PR 03-SEP-1999; 99DE-1042123.
 PR 03-SEP-1999; 99DE-1042125.
 PA (BADI) BASF AG.
 PI Pompejus M, Kroegeer B, Schroeder H, Zelder O, Haberhauer G;
 P-PSDB; AAB79287.
 DR MPI: 2001-061975/07.
 DR P-PSDB; AAB79287.
 XX
 PT New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
 PT metabolism and oxidative phosphorylation protein for production or
 PT modulation of production of fine chemicals e.g. amino acids,
 PT carbohydrates or enzymes -
 PS
 PS Claim 3: Page 274-275; 1246pp; English.
 CC AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
 CC metabolism and oxidative phosphorylation (SMP) proteins given in
 CC AAB79243 to AAB 79633 which are involved in carbon metabolism and
 CC energy production. The C. glutamicum SMP gene can be used in vectors
 CC (II) for expression in host cells and production or modulation of
 CC production of fine chemicals, such as, an organic acid, a proteinogenic
 CC or nonproteinogenic amino acid (preferred), a purine or pyrimidine base,
 CC a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty
 CC acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a
 CC cofactor, a polypeptide, or an enzyme. The presence of (I) or SMP proteins
 CC (III) encoded by them are used for diagnosing the presence or activity of
 CC Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells
 CC containing them are used to map genomes of organisms related to
 CC C. glutamicum. identify and localise C. glutamicum sequences of interest,
 CC in evolutionary studies, in determining SMP protein regions required
 CC for function, in modulating SMP protein activity, in modulating the
 CC metabolism of sugars, and in modulating high-energy molecule production
 CC in a cell (i.e. ATP, NADPH).

XX Sequence 944 BP; 222 A; 213 C; 276 G; 233 T; 0 other;

Query Match 43.7%; Score 944; DB 22; Length 944;
Best Local Similarity 100.0%; Pred. No. 6.8e-291;
Matches 944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1143 GGTACGATTTCCCTTATCTGATTTCTTCCCTAAAGACAGCTTCCAGGTGATATC 1202
DB 1 GGTACGATTTCCCTTATCTGATTTCTTCCCTAAAGACAGCTTCCAGGTGATATC 60
QY 1203 AACGTTGCCACATTTGGTGCAGCTACACCGGTGAGTATCCGGTGCAGGTATGCT 1262
DB 61 AACGTTGCCACATTTGGTGCAGCTACACCGGTGAGTATCCGGTGCAGGTATGCT 120
QY 1263 GCACACATCGAAATATTTTGGCTCATGTGAGGAGGAGGAGGAGTCCCTTCCCTGAT 1322
DB 121 GCACACATCGAAATATTTTGGCTCATGTGAGGAGGAGGAGGAGTCCCTTCCCTGAT 180
QY 1323 CGGATGCTCAAGGCACACGACGCGTAAAGTTGAGCTCGGTGATAGAGCTACACATAC 1382
DB 181 CGGATGCTCAAGGCACACGACGCGTAAAGTTGAGCTCGGTGATAGAGCTACACATAC 240
QY 1383 GTGAGAGAGATGTGGCTATTTACCTGAAATACGCTGCTATTTTGAACAGAGTGGCG 1442
DB 241 GTGAGAGAGATGTGGCTATTTACCTGAAATACGCTGCTATTTTGAACAGAGTGGCG 300
QY 1443 GATAGGATGCGGTGTTTACTGTGATACCGCATGCAATGTGGCATGCGAGGTAC 1502
DB 301 GATAGGATGCGGTGTTTACTGTGATACCGCATGCAATGTGGCATGCGAGGTAC 360
QY 1503 ATGAGAAATCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1562
DB 361 ATGAGAAATCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
QY 1563 AATGCGTGGCTCATGATGTGTTGGGCAAAAGTGTGATGCAAAAGGAGGAGGAGGAG 1622
DB 421 AATGCGTGGCTCATGATGTGTTGGGCAAAAGTGTGATGCAAAAGGAGGAGGAGGAG 480
QY 1623 ATGTGTGGCATGTGGTGTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1682
DB 481 ATGTGTGGCATGTGGTGTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 1683 CAATTCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1742
DB 541 CAATTCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
QY 1743 ATGCTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1802
DB 601 ATGCTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY 1803 AATGCGGCGGCTGCGGCTGATCAATGCTGATACGATACCGATCCGAAAGGTTCCGAG 1862
DB 661 AATGCGGCGGCTGCGGCTGATCAATGCTGATACGATACCGATCCGAAAGGTTCCGAG 720
QY 1863 CAGCTAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1922
DB 721 CAGCTAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 1923 AATGCGGTGCGATCCACCAACCATCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1982
DB 781 AATGCGGTGCGATCCACCAACCATCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 1983 GCCACCCGAAACCGCTTTTGGTGGAGAGTAGAGGAGGAGGAGGAGGAGGAGGAG 2042
DB 841 GCCACCCGAAACCGCTTTTGGTGGAGAGTAGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 2043 ATAGAGAAATTTCTTCTACTCATATGATATGATACACTGCTGTT 2086
DB 901 ATAGAGAAATTTCTTCTACTCATATGATATGATACACTGCTGTT 944

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RESULT 11

AA15848
ID AA15848 standard; DNA; 875 BP.

XX AA15848;

XX 16-JAN-2002 (first entry)

DE C. glutamicum pyruvate oxidase, poxb, mutagenic fragment.

KM Transketolase, tkt; ds: L-amino acid fermentation; animal nutrition;

KW human medicine; pharmaceutical industry; pyruvate oxidase: poxb.

XX Corynebacterium glutamicum.

PN MO200168894-A1.

PD 20-SEP-2001.

XX 05-JUL-2000; 2000MO-EP06305.

XX 17-MAR-2000; 2000US-0528196.

PA (DEGS) DEGUSA AG.

PI (UYNA-) UNIV NAT IRELAND.

PI Dunican LK, McCormack A, Stapleton C, Burke K, Moeckel B;

PI Thierbach G;

DR WPI; 2001-656800/75.

PT Preparation of L-amino acids, e.g. L-lysine, L-threonine or

PT L-iso-leucine, useful in animal nutrition or in human medicine,

PT comprises fermenting L-amino acid-producing coryneform bacteria with

PI amplification of the tkt gene

XX Example 7; Page 48; 53pp; English.

PS The invention relates to the preparation of L-amino acids comprising

CC fermenting L-amino acid-producing coryneform bacteria which

CC overexpresses a gene e.g. that for transketolase, tkt. Also

CC included are transformed coryneform microorganisms harbouring the

CC plasmid pEC-R18mb2 which contains the tkt gene. The method is useful for

CC the fermentative preparation of L-amino acids, i.e. L-lysine, L-threonine

CC and L-iso-leucine, in which at least the tkt gene is amplified, in human

CC L-threonine and L-iso-leucine are useful in animal nutrition, in human

CC medicine and in the pharmaceuticals industry. The present sequence

CC is a fragment of the gene for pyruvate oxidase, poxb, which was used

CC to eliminate the poxb gene by insertional mutagenesis in a strain

CC expressing with tkt in order to further increase yields of L-amino acids.

XX Sequence 875 BP; 190 A; 193 C; 266 G; 226 T; 0 other;

Query Match 40.5%; Score 875; DB 22; Length 875;
Best Local Similarity 100.0%; Pred. No. 7.7e-269;
Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 705 TCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 764
DB 1 TCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
QY 765 ACCATGCGCGGATTAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 824
DB 61 ACCATGCGCGGATTAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 825 GCAGGTGACGAGTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 884
DB 121 GCAGGTGACGAGTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 180
QY 885 GATCCTACTGAGGCTGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 944
DB 181 GATCCTACTGAGGCTGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 945 TTCGCGGTGCGGCGGTAAAGATGCTGCGCGCGAGGAGTGTGAGATTCGCGGAGAGATT 1004

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XX 02-MAY-2001.
 PD 14-OCT-2000; 2000EP-0122505.
 XX 28-OCT-1999; 99DE-1051975.
 XX (DEGS) DEGUSA AG.
 XX Moeckel B, Weissenborn A, Pfeifferle W, Puhler A, Kalinowski J;
 PI Bathe B, Dusch N;
 XX WPI; 2001-309855/33.
 DR
 XX
 XX
 PT New Coryneform glutamicum poxb pyruvate oxidase polynucleotide useful
 PT for insertional mutation, producing strains with increased production
 PT of amino acids
 XX
 PS Disclosure; Page 18; 21pp; German.
 XX
 CC This invention describes a novel polynucleotide (I) which is used for
 CC insertional mutagenesis of the poxb gene in coryneform bacteria. The poxb
 CC gene can be used for fermentative production of L-amino acids,
 CC specifically L-lysine, which is used in human medicine, foods and
 CC especially animal nutrition. (I) is also useful as a source of probes and
 CC primers for isolation of related sequences. Cells in which the poxb gene
 CC is suppressed produce higher yields of L-amino acids. This sequence
 CC encodes a fragment of the pyruvate oxidase (E.C. 1.2.2.2) poxb gene from
 CC Corynebacterium glutamicum ATCC13032 found in plasmid pCR2.1-Topo which
 CC is described in the invention.
 CC
 XX
 SQ Sequence 875 BP; 190 A; 193 C; 266 G; 226 T; 0 other;

Query Match 40.5%; Score 875; DB 22; Length 875;
 Best Local Similarity 100.0%; Pred. No. 7.7e-269;
 Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 705 TGGCGATGGTGAATGAGTGGTGAAGAGGATGAGGATTTGATTCAGGATTCATGCC 764
 DB 1 TGGGAGATGGTGAATGAGTGGTGAAGAGGATGAGGATTTGATTCAGGATTCATGCC 60
 OY 765 ACCATGGCGGGTAAAGGTGTGTGAGTGTGATTCCTGTGATTCGATTCAGGAGAC 824
 DB 61 ACCATGGCGGGTAAAGGTGTGTGAGTGTGATTCCTGTGATTCGATTCAGGAGAC 120
 OY 825 GCAGGTGAGGATCTTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 884
 DB 121 GCAGGTGAGGATCTTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 180
 OY 885 GATCCTACTGAGGATCGACGCTGTGTGAGGATTCATTCAGGATTCATTCATTCATTC 944
 DB 181 GATCCTACTGAGGATCGACGCTGTGTGAGGATTCATTCAGGATTCATTCATTCATTC 240
 OY 945 TTTCTGGGTTGGGGGGTGAAGAATGCTCGCGGAGGTGTGAGTGGGAGGAGATTT 1004
 DB 241 TTTCTGGGTTGGGGGGTGAAGAATGCTCGCGGAGGTGTGAGTGGGAGGAGATTT 300
 OY 1005 AAATCACCAGATCGGGCATCGCTGTGTGAGGATTCATTCAGGATTCATTCATTC 1064
 DB 301 AAATCACCAGATCGGGCATCGCTGTGTGAGGATTCATTCAGGATTCATTCATTC 360
 OY 1065 GAGTTCGGCATGTCTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1124
 DB 361 GAGTTCGGCATGTCTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
 OY 1125 GATCTGCGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 1184
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 DT 05-JUL-2002 (first entry)
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 KW animal nutrition; ds.
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 PD 11-APR-2002.
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 PR
 XX (DEGS) DEGUSA AG.
 XX
 XX Dusch N, Herrmann T, Thierbach G;
 PI
 DR WPI; 2002-363950/40.
 XX
 PT Fermentative production of D-pantothenic acid (I), useful e.g. in
 PT animal nutrition, from coryneform bacteria with reduced activity of the
 PT pyruvate oxidase gene
 XX
 PS Example 3; Page 16; 28pp; German.
 XX
 CC The invention relates to the fermentative production of D-pantothenic
 CC acid (I) by growing a (I)-producing coryneform bacterium in which the
 CC activity of at least the sequence poxb (ABL58754, ABL58756) encoding
 CC pyruvate oxidase (AB58755, EC 1.2.2.2) has been weakened, especially
 CC switched off. (I) is then recovered from medium or cells. (I) is a
 CC vitamin useful in human medicine, the pharmaceutical and food industries
 CC and particularly in animal nutrition. Reducing the activity of poxb
 CC improves fermentative production of (I). The present sequence is that of
 CC a polynucleotide fragment of the poxb gene, useful in examples of the
 CC invention.
 CC
 XX
 SQ Sequence 875 BP; 190 A; 193 C; 266 G; 226 T; 0 other;

GenCore version 5.1.6
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

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1	2160	100.0	2160	6	AX137665 Sequence
2	2160	100.0	2160	6	AX250315 Sequence
3	2160	100.0	2160	6	AX253245 Sequence
4	2160	100.0	2160	6	AX253251 Sequence
5	2160	100.0	2160	6	AX404607 Sequence
6	2160	100.0	2160	6	BD014868 Sequence
7	2160	100.0	3248	6	AX404610 Sequence
8	2160	100.0	320550	1	AP005282 Sequence
9	2160	100.0	349980	6	AX127152 Sequence
10	1860	86.1	1860	6	AX064959 Sequence
11	1737	80.4	1737	6	AX122957 Sequence
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ALIGNMENTS

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JOURNAL In the preparation of l-lysine
Patent: EP 1096013-A 1 02-MAY-2001;
Degussa AG (DE)
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 1 Dunican, L.K., Stapleton, C., Burke, K., Moekel, B. and Thierbach, G.
 Process for the fermentative preparation of L-amino acids with
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 1 Burke, K., Sahm, H., Eggeling, L., Moritz, B., Dunican, L.K.,
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 Process for the fermentative preparation of L-amino acids with
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 ORGANISM Corynebacterium glutamicum
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 REFERENCE 1 (bases 1 to 2160)
 AUTHORS Doush, N., Baate, B., Kalinowski, J., Alfred, Puehler, Meckel, V., Weisenborn, A. and Pfeifferle, M.
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RESULT 7
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 Corynebacterium glutamicum
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 REFERENCE
 1 Dusch, N., Herrmann, T. and Thierbach, G.
 Process for the fermentative preparation of D-pantothenic acid
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 Patent: WO 0229020-A 4 11-Apr-2002;
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FEATURES	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL
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Db	114861	GTTGTGAGCAGGATGATGATGATGATGATGATGATGATGATGATGATGATG	114802						
QY	781	GTTGTGAGCAGGATGATGATGATGATGATGATGATGATGATGATGATGATG	840						
Db	114801	GTTGTGAGCAGGATGATGATGATGATGATGATGATGATGATGATGATGATG	114742						
QY	841	ATTCACATTCACATATTTCTGTCGACATCTGTCGATGATGATGATGATGATG	900						
Db	114741	ATTCACATTCACATATTTCTGTCGACATCTGTCGATGATGATGATGATGATG	114682						
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QY 1381 ACCTGCGAAGAGCTGTGCTATTACACCTGATAGTTCCTCTATTGAAACGAGCTGG 1440
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Db 114201 ACCTGCGAAGAGCTGTGCTATTACACCTGATAGTTCCTCTATTGAAACGAGCTGG 114142
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LOCUS
DEFINITION Sequence 7068 from Patent EP1108790.
ACCESSION AX127152 AX114121
VERSION AX127152.1 GI:14041140
KEYWORDS
SOURCE
ORGANISM
Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinomycetales;
Corynebacteriaceae; Corynebacteriidae; Corynebacterium.
REFERENCE
1 Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K.,
Tokoi, H., Tateshi, N., Senoh, A., Ikeda, M. and Ozaki, A.
Novel polynucleotides
Patent: EP 1108790-A 7068 20-JUN-2001;
JOURNAL KYOMA HAKKO KOGYO CO., LTD. (JP)
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QY 121 TTGGTTTCGAGGGGCTTAACCAACCAAGCTGCGCCAGCAACGAGAAATCCCAAAAGT 180
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 Matches 1860; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DEFINITION Sequence 2873 from Patent EP1108790.
 ACCESSION AX122957
 VERSION AX122957.1 GI:1404045
 KEYWORDS
 SOURCE
 ORGANISM
 Corynebacterium glutamicum
 Corynebacterium glutamicum
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacteriaceae; Corynebacteriales; Corynebacterium.
 1
 NAKAGAWA, S., MIZOGUCHI, H., ANDO, S., HAYASHI, M., OCHIAI, K.,
 YOKOI, H., TATEISHI, N., SENOH, A., IKEDA, M. and OZAKI, A.,
 Novel polynucleotides
 Patent: EP 1108790-A 2873-20-JUN-2001;
 KYOMA HAKKO KOGYO CO., LTD. (JP)


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PD JP 2002191370-A/2873
PD 09-JUL-2002
PF 15-DEC-2000 JP 2000405096
PI SATOSHI NAKAGAWA, HIROSHI MIZOGUCHI, SEINO ANDO, MIKIO HAYASHI,
PI KEIKO OCHIAI,
PI HARUHIKO YOKOI, NAKO TATEISHI, AKIHIRO SENOO, MASATO IKEDA, AKIO
PI OZAKI
PC C12N15/09, C12N15/09, C07K14/34, C07K16/12, C07K16/40, C12M1/00, PC
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PC C12N1/19, C12N1/21, C12N5/10, C12N9/00, C12N9/02, C12N7/40, C12P13/
PC 04, C12P13/08,
PC C12P19/00, C12P19/34, C12P21/02, C12Q1/37, C12Q1/68, G01N33/53, PC
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PC C12N5/00, C12N15/00
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Matches 1737; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
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 LOCUS Sequence 5 from Patent WO0168894.
 DEFINITION AX250317
 ACCESSION AX250317 GI:15984085
 VERSION AX250317.1
 KEYWORDS
 SOURCE
 ORGANISM
 Corynebacterium glutamicum
 Corynebacterium glutamicum
 Bacteria: Actinobacteria: Actinobacteridae: Actinomycetales:
 Corynebacterineae: Corynebacteriaceae: Corynebacterium.
 REFERENCE
 1 Dunican, L.K., Stapleton, C., Burke, K., Moeckel, B. and Jhierbach, G.
 AUTHORS
 TITLE
 JOURNAL
 Degussa AG (DE) ; National University of Ireland (IE)
 FEATURES
 Location/Qualifiers

source 1. 875
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 ORIGIN

Query Match 40.5%; Score 875; DB 6; Length 875;
 Best Local Similarity 100.0%; Pred. 4e-232;
 Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Oy 825 GCAGGTGAGGCTACTTATTCACATATTCCTGTGCGACTCTGTGTTCCCG 884
 Db 121 GCAGGTGAGGCTACTTATTCACATATTCCTGTGCGACTCTGTGTTCCCG 180
 Oy 885 GATCTACTGAGGCTGAGGCTGTGTGAGGCGATTAACAACGCTAAGTGTCTACTTTG 944
 Db 181 GATCTACTGAGGCTGAGGCTGTGTGAGGCGATTAACAACGCTAAGTGTCTACTTTG 240
 Oy 945 TTCTGCGGTGCGGCGTGAAGAAATGCTCGCGCGAGGTGTTGAGATTGGCGGAGAAATT 1004
 Db 241 TTCTGCGGTGCGGCGTGAAGAAATGCTCGCGCGAGGTGTTGAGATTGGCGGAGAAATT 300
 Oy 1005 AAATACCCGATCGGCGCTGTGCGGTGATAGAGATCCAGCATGAGATCCGTTT 1064
 Db 301 AAATACCCGATCGGCGCTGTGCGGTGATAGAGATCCAGCATGAGATCCGTTT 360
 Oy 1065 GAGGTGCGCATGTCGTGCGCTGCTTTGTTACGCGCGCTGCGTGTGATGCTCAATGAGCG 1124
 Db 361 GAGGTGCGCATGTCGTGCGCTGCTTTGTTACGCGCGCTGCGTGTGATGCTCAATGAGCG 420
 Oy 1125 GATGTGCTGATTCATTTGGGTGAGGATTTCCCTATTCATTTCTTCTCTAAAGAAC 1184
 Db 421 GATGTGCTGATTCATTTGGGTGAGGATTTCCCTATTCATTTCTTCTCTAAAGAAC 480
 Oy 1185 GTTCCCGAGGTGATTCACAGGTGCGCATGTCGACGTACACAGGTGAAGATCCG 1244
 Db 481 GTTCCCGAGGTGATTCACAGGTGCGCATGTCGACGTACACAGGTGAAGATCCG 540
 Oy 1245 GATGTCCTCTCTGTCGATGCTGCAAGGCAACAGGCTAAGTGAAGTGAAGTGAAGTGA 1304
 Db 541 GATGTCCTCTCTGTCGATGCTGCAAGGCAACAGGCTAAGTGAAGTGAAGTGAAGTGA 600
 Oy 1365 GAGACGTACACATTAACGTGCAAGACATGTCCTTACCTGATTAACCTGCTCT 1424
 Db 661 GAGACGTACACATTAACGTGCAAGACATGTCCTTACCTGATTAACCTGCTCT 720
 Oy 1425 ATTTTGAACGAGTGGGAGTAAGGATGCGTGTTCCTGTGATACCGCATGTGCAAT 1484
 Db 721 ATTTTGAACGAGTGGGAGTAAGGATGCGTGTTCCTGTGATACCGCATGTGCAAT 780
 Oy 1485 GTGTGCGATGCGAGTACATGAGATCCGAGGGAACGCGCATTTGTGGTTCAATC 1544
 Db 781 GTGTGCGATGCGAGTACATGAGATCCGAGGGAACGCGCATTTGTGGTTCAATC 840
 Oy 1545 CGCCACGCGACGATGGCTAATGCGTTCCTCATGC 1579
 Db 841 CGCCACGCGACGATGGCTAATGCGTTCCTCATGC 875

Search completed: October 3, 2003, 17:41:27

Tue Oct 7 07:11:10 2003

us-09-965-825-1.rge

Page 20

Job time : 7717 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 3, 2003, 15:10:07 : Search time 4096 Seconds

(without alignments)
12816.814 Million cell updates/sec

Title: US-09-965-825-1

Perfect score: 2160

Sequence: 1 ttagagcgatctctgtgaggg.....gtgcacatgatgcct 2160

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estbm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estro:*
7: em_estro:*
8: em_hci:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	183	8.5	601	BH010685	BH010685 ep67h04.9
2	150.2	9.06	29	CNS0104W	AL153073 Anopheles
3	109	5.0	1451	B2571467	B2571467 msh2.1902
4	105.8	4.9	487	CD288304	CD288304 3_p8.abd

5	104.8	4.9	731	29	CNS01PEV	AL141752 Anopheles
6	100.4	4.6	375	29	CNS0713Y	AL611872 Anopheles
7	100	4.6	837	29	B2571498	B2571498 msh2.1917
8	95.8	4.4	538	9	AM036130	AM036130 EST724506
9	91.6	4.2	1037	29	B2559326	B2559326 pac2.164
10	91.2	4.2	274	10	B627542	B627542 CC-est1CL
11	89.8	4.2	550	12	BM534496	BM534496 fwr8h06.y
12	87.4	4.0	769	29	B2549561	B2549561 pac31-60_
13	85.2	3.9	879	29	B2571612	B2571612 msh2.1969
14	72.2	3.3	299	28	BH241614	BH241614 AUL1B19TF
15	70.8	3.3	1862	28	BH770875	BH770875 LLMGta961
16	69.8	3.2	467	9	AM036129	AM036129 EST274505
17	68	3.1	484	12	BM137811	BM137811 WHE0471.A
18	59.6	2.8	1202	29	B2579361	B2579361 msh2.6320
19	59.2	2.7	475	9	A1097766	A1097766 uc35f02.y
20	59.2	2.7	504	9	A1931656	A1931656 u171h04.y
21	59.2	2.7	561	4	BX516379	BX516379 RFPD Mus
22	59.2	2.7	577	10	BB638384	BB638384 BB638384
23	59.2	2.7	630	14	BY705708	BY705708 BY705708
24	59.2	2.7	701	10	BB653627	BB653627 BB653627
25	59.2	2.7	757	14	CB950802	CB950802 AGENCOURT
26	59.2	2.7	815	12	B1554388	B1554388 603235891
27	59.2	2.7	827	9	AU079796	AU079796 AGENCOURT
28	59.2	2.7	918	12	B1690622	B1690622 603314217
29	59.2	2.7	1015	13	BQ960366	BQ960366 AGENCOURT
30	59.2	2.7	1974	11	AK005505	AK005505 Mus muscu
31	59.2	2.7	1976	11	AK050078	AK050078 Mus muscu
32	59.2	2.7	2615	11	AK041686	AK041686 Mus muscu
33	58	2.7	539	9	AW217660	AW217660 EST296374
34	58	2.7	639	10	BG130411	BG130411 EST476057
35	58	2.7	766	12	B1925329	B1925329 EST45218
36	58	2.7	770	12	B1935305	B1935305 EST555194
37	58	2.7	802	12	B1935831	B1935831 EST555720
38	57.6	2.7	845	10	BE282914	BE282914 601100571
39	57	2.6	593	9	AL865382	AL865382 AL865382
40	57	2.6	939	29	CNS01KC4	AL148149 Anopheles
41	55.8	2.6	335	13	BY141680	BY141680 BY141680
42	55.8	2.6	360	13	BY320483	BY320483 BY320483
43	55.8	2.6	362	13	BY147322	BY147322 BY147322
44	55.8	2.6	380	13	BY321497	BY321497 BY321497
45	55.8	2.6	430	14	CA544748	CA544748 K0103E03-

ALIGNMENTS

RESULT 1
BH010685
LOCUS
DEFINITION
ep67h04.g1 TO1000 Brassica oleracea genomic clone ep67h04 5',
genomic survey sequence.

ACCESSION
BH010685
VERSION
BH010685.1 GI:13956880
KEYWORDS
SOURCE
GSS.
ORGANISM
Brassica oleracea

REFERENCE
AUTHORS
Katarai,M., O'Shaughnessy,A., Palmer,L., Bahret,A., Baker,J., Ballja
V., Bell,M., Cummins,D.M., King,L., Kirchoff,K., Kuhl,K., Miller
B., Nascimento,L., Preston,R., Rodriguez,S., Santos,L., Shah,R.,
Vill.M.D., Zulueta,T., Bal,H., Dedhia,N. and McCombie,W.R.

TITLE
JOURNAL
COMMENT
Whole Genome Shotgun Reads from Brassica oleracea

Unpublished
Contact: W. Richard McCombie
Iltia Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org

by F. H.

stitut

CGGATCG 506
|||
CGGATCG 506

CTAGCCAT 626
|||
CCGCCAC 270

SCATTTTG /46
|||
CAGTCTC 389

11
GGCGCGC 509

1 1 1 1 1
GCTGCTG 628

Db 629 GAATTTGGCGGAAACCTGAAA-CCCCGATGTGTCACCGCTCGCGGGCAAGAGACAGCTC 687

QY 1047 CAGCATGAGAAATCCCTTTGAGTGGCGCATGTCTGGCCCTGTTGGTTAGCGGCGCTGCTG 1106

Db 668 GAATACGATTAACCCCTGACGATGTAGCATGACCGGGGATGCGGTTTTCCTCGCGCTTC 747

QY 1107 GATGCGTCAATGACGCGGATCTGCTGATTTCTATGCGGTACGATTTCCCTTA--TTCT 1163

Db 748 CACACCATGATGAACGCCGACACGCTGATBCTGCTGGCACCACCATTTCCCTACCGCGCG 807

QY 1164 GATTTCTCTCTTAAGAACAAGCTTCCAGGTGATATCAACGGTGGCGACATTTGCTGA 1223

Db 808 TTATACCCGACGATGCTAAATCATTCATTCATATCAACCCGCGCAGATCGGCGCG 867

QY 1224 CGTACACGCGTGAATATCCGCTGACCGGTGA 1255

Db 868 CACAGCAAGTGTGATATGCGCTGCTGGCGM 899

RESULT 3 B2571467/c

LOCUS B2571467 1451 bp DNA linear GSS 17-DEC-2002

DEFINITION msh2_1902.y2 msh Pseudomonas aeruginosa genomic clone msh2_1902.

ACCESSION B2571467

VERSION B2571467.1 GI:27206528

KEYWORDS GSS.

SOURCE Pseudomonas aeruginosa

ORGANISM Pseudomonas aeruginosa

REFERENCE 1 (bases 1 to 1451)

AUTHORS Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M., Burns,J.L., Kaul,R. and Olsen,M.V.

TITLE Whole-Genome-Sequence Variation among multiple isolates of Pseudomonas aeruginosa library

JOURNAL J. Bacteriol., (2002) In press

COMMENT Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu

Class: Shotgun.

FEATURES

source 1..1451

/organism="Pseudomonas aeruginosa"

/mol_type="genomic DNA"

/strain="MSH"

/db_xref="taxon:287"

/clone="msh2_1902"

/clone_lib="msh"

/note="Environmental isolate. Whole genomic shotgun library."

BASE COUNT 271 a 358 c 394 g 263 t 165 others

ORIGIN

Query Match 5.0%; Score 109; DB 29; Length 1451;

Best Local Similarity 52.1%; Pred. No. 9,4e-20;

Matches 264; Conservative 0; Mismatches 242; Indels 1; Gaps 1;

QY 1447 AGATGCGGTGTTTCTGATACCGCATGTGCGATGCGAGATCATCG 1506

Db 599 AGAGCGCCCTTTCACNNCGACGTCGCGCATGTCTGCTGTTGCTCACATC 540

QY 1507 AGAATCGGAGGAGGAGCGGCGACTTTGTGGGTTCAATCCGACGACGATGCTAATG 1566

Db 539 CCTACAGCGGCAACCGCTGACCTTCACGACA-TGTCGCCGCGACACATGGCGACGG 481

QY 1567 CGTGGCTGATGCGGATTTGGTGGCAAGTGTGATGCAACCGCGAGTGGATGCT 1626

Db 480 CCATGCCCAAGGCGCTGGGCTGAAGAAGGCTTACTCCGAGCCGACGATATCTGATCT 421

QY 1627 GTGGCGATGGTGGTGGGCAATGCTGCGGGTGAGCTTTGACCGTTAAGTCCAGCAC 1686

Db 420 CGGCGAGGCGGCGCTGCGCATGCTGCTGGCGACCTGCTGACGCGCATCCAGGAAAAAC 361

QY 1687 TTCGCTGAAGGCTGTGTGTGTAAACAAGTTCTTTGGCATGTGAGCTTGGAGATGC 1746

Db 360 TGCGGATCAACGATAGTGTGTGTGAACATGCTGCTGGAACCTGTGAGCTGGAACAGA 301

QY 1747 TCGTGAAGGACAGCCAGATTTTGACTACCATGAGGAAGTAATTTGCGACAGATTG 1806

Db 300 AGGTGAGGCGCTCTGACACAACTACACCGACCTGCTCAACCCGACCTGCGCTGCG 241

QY 1807 CGGCGGCTCGGCGATCAATGCGTACGATACCGATCGAAGAAGTTGCGGACGAC 1866

Db 240 CGGAAGTATGCGCTTCCACGACGACGCAAGGTGAGCGCTCGAGAGCTCGAGCGGCG 181

QY 1867 TAGCTGAGGCAATTTGCGATATCTGACCTGTACTGATGATATGTCACGATCTAATG 1926

Db 180 TGCAAGAGTTCCTCGCCACCGCGCTGCTGGAGCTGATACATACCAACCTCGCG 121

QY 1927 CGCTGTGATCCCAACCAATTCACGT 1953

Db 120 AGCTGTGATGCTCGCCGAAGATCGAGT 94

RESULT 4 CD288304/c

LOCUS CD288304 487 bp mRNA linear EST 27-MAY-2003

DEFINITION 3_P8.abd POE14_(Day_14_pregnant_ovine_endometrium) Ovis aries CDNA, mRNA sequence.

ACCESSION CD288304

VERSION CD288304.1 GI:31086347

KEYWORDS EST.

SOURCE Ovis aries (sheep)

ORGANISM Ovis aries

REFERENCE 1 (bases 1 to 487)

AUTHORS Gray,C.A., Adelson,D.L. and Spencer,T.E.

TITLE Ovine ESTs

JOURNAL Unpublished

COMMENT Contact: Thomas E. Spencer
Center for Animal Biotechnology and Genomics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471, USA

FEATURES

source 1..487

/organism="Ovis aries"

/mol_type="mRNA"

/db_xref="taxon:9940"

/sex="female"

/tissue_type="endometrium"

/dev_stage="Day 14 pregnant"

/clone_lib="POE14_(Day_14_pregnant_ovine_endometrium)"

/note="Organ: uterus; Vector: Triplex2; Site:1; EcoRI; Site:2; XhoI; Non-normalized library; sequenced 5' with Triplex2 primer (CTCGAATATGCGACGACG). Library constructed by Clontech with total RNA extracted using the Trizol method and pooled from 5 females."

BASE COUNT 99 a 135 c 145 g 108 t

ORIGIN

Query Match 4.9%; Score 105.8; DB 14; Length 487;

Best Local Similarity 54.5%; Pred. No. 4.3e-19;

Matches 212; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

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QY      447 ATTGAGTGGGTGCACGTTCCGAATGAGGAACGGCGCGCTTTTCACGCCGGTGGGAATCG 506
      11 111111 11 111111 111111 111111 111111 111111 111111 111111
Db      444 ATGAGTGGATGTCTCCACCGCCACGAAGAAGTGGCGGCTTTGCCGCTGGCGCTGAAGCA 385
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QY      507 TTGATCACTGGGGAGCTGGCAGATATGTGCTTCTTTGCTGCTTCTTGAACACACACTG 566
      11 111111 111111 111111 111111 111111 111111 111111 111111 111111
Db      384 CAACCTTAGCGGAACACTGGCGGTCTGCGCGGATCTGCGGCCCGCCGCAACTGCACTTA 325
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QY      567 ATTACAGGCTTTATGATTCGACATCGAATGTGCGCAAGGTGTTGGCCATCGCTAACCAT 626
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Db      324 ATCAAGGGCCTGTGTGATTCGCCACCGCATACAGTTCCGTTACTGGCGATTCGCGCTCAT 265
      11 111111 111111 111111 111111 111111 111111 111111 111111 111111
QY      627 ATTCCGAGTCCCGACAGTTGTTGCGAGCTTCTTCCAGAAAACGATCCGAGATTGTTT 686
      111111 111111 111111 111111 111111 111111 111111 111111 111111
Db      264 ATTCCTCCAGGAAATGTGCGACGGCTATTCTCCAGAAAACCCACCAAGAGCTATTC 205
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QY      687 AAGGAATGCTGTGTACTGCGAGATGTGTGATGTGTGAGCAGGGTGAACGATTTTG 746
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Db      204 CCGGATGTAGTACTATTGCGAGCTGTTCCAGGCCCGGAGCAGATCCACAAAGTACTG 145
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QY      747 CATCAGCGATTCAGTCCACATGCGGGGTAAAGTGTGCGGTGATGATTCCTGGT 806
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Db      144 GCGATTGCCATGCGCAAGCGGTGCTTAACCGTGGCGTTTCGTTGTCTGTACCAAGC 85
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QY      807 GATATCGCTAAGGAAGACCGCAGGTACGG 835
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RESULT 5
CONS01FEV 731 bp DNA linear GSS 01-JUN-2001
LOCUS Anopheles gambiae GSS 17 end of clone 04P15 of NotreDame1 library
DEFINITION from strain PEST of Anopheles gambiae (African malaria mosquito),
genomic survey sequence.
ACCESSION AL141752.1 GI:6999870
VERSION AL141752.1 GI:6999870
KEYWORDS GSS.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles
REFERENCE 1 (bases 1 to 731)
AUTHORS Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
TITLE Direct Submission
JOURNAL Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
Roux, Paris 75015, France
COMMENT This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
Pasteur.
FEATURES
source location/Qualifiers
1..731
/mol_type="genomic DNA"
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="04P15"
/clone_lib="NotreDame1"
/note="end : 17"

BASE COUNT 157 a 222 c 215 g 127 t 10 others

Query Match 4.9%; Score 104.8; DB 29; Length 731;
Best Local Similarity 53.0%; Pred. No. 1e-18;
Matches 319; Conservative 6; Mismatches 270; Indels 7; Gaps 5;

```

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QY      447 ATTGAGTGGGTGCACGTTCCGAATGAGGAACGGCGCGCTTTTCACGCCGGTGGGAATCG 506
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Db      133 ATGGAATGATGGCCGACCCGCCCATGGAAGAGTGTGCCGCTTGGCCGCAAT -NGNAGCA 191
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QY      507 TTGATCACTGGGGAGCTGGCAGATATGTGCTTCTTTGCTGCTTCTTGAACACACACTG 566
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QY      567 ATTACAGGCTTTATGATTCGACATCGAATGTGCGAAGGTGTTGGCCATCGCTAACCAT 626
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Db      252 ATCAAGGGCCTTTTGCAGCTCAACCGTAAACAGCTTCGCGTCCGGATTCGCCGCCAC 311
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QY      627 ATTCCGAGTCCCGACAGATGTGTGAGCTTCTTCCAGAAAACGATCCGAGATTGTTT 686
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QY      687 AAGGAATGCTGTGTACTGCGAGATGTGTGATGTGTGATGAGCAGGGTGAACGATTTTG 746
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Db      371 CGTGAATGCGACCATTTCTGAACTGTGTTCAATCCCGGAGCA -RATCCCGCAGTCTG 429
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QY      747 CATCAGCGATTCAGTCCACCATGCGGGGTAAAGTGTGCGGTGATGATTCCTG 806
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Db      430 GCGATCGCATGCGCAAGCGCGTGTGAATCGCGGGGTGCCGTTATCCCGGCC 489
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QY      807 GATATCGCTAAGGAAGACCGCAGGTGACGTTACTTATTCATTCATTTCTTTCG 866
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Db      490 GACGTGGCGCTAAGGCCCGCGCGGAGGAGCCAGCAGCTGATACCGGCC -G 546
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QY      867 ACTCTGTGTGTCTTCCCGGATCCTACTGAGGCTGACGCGTGTGAGGCGATTAAAC 926
      11 111111 11 111111 11 111111 111111 111111 111111 111111
Db      547 CAGCCGCTGTGTAGCGCAGCGGAGAGAGACTTAAARCTGGCCGASTGTGCTGCTTAC 606
      11 111111 111111 111111 111111 111111 111111 111111 111111
QY      927 GCTAAGTCTGTCACTTGTGTGCGGTGCGGGGTGAAGATCTCGCGCAGGTGTTG 986
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Db      607 GCAGCAATATGCGCCTKATGTGCGCAGCGGTGTG -CGGGCGGATTAAGAARCTKCTG 665
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QY      987 GAGTGGCGGAGAAAGTTAATACCGATGCGGATCGGTGCTGTTAAGCATCATC 1046
      111111 111111 111111 111111 111111 111111 111111 111111 111111
Db      666 GAATTTGCGGAAAGCTGAASCCGGAATTTGCACGCCCTGCGCGCAAGAGCAGTCT 725
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QY      1047 CA 1048
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Db      726 GA 727

RESULT 6
CONS0713Y/c 375 bp DNA linear GSS 03-OCT-2001
LOCUS Anopheles gambiae GSS sp6 end of clone 32N20 of library NotreDame1
DEFINITION from strain PEST of Anopheles gambiae (African malaria mosquito),
genomic survey sequence.
ACCESSION AL611872.1 GI:15963295
VERSION AL611872.1 GI:15963295
KEYWORDS GSS.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles
REFERENCE 1 (bases 1 to 375)
AUTHORS Roth,C.W., Brey,P.T., Ke,Z. and Collins,F.H.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
2 (bases 1 to 375)
Roth,C.W., Brey,P.T., Ke,Z. and Collins,F.H.
Direct Submission
Submitted (03-OCT-2001) BBMI, Institut Pasteur, 25, rue du Dr.
Roux, Paris 75015, France
COMMENT This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the

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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 214)
van der Hoeven, R.S. and Tanksley, S.D.
ESTs from a tomato flower library
Unpublished
Contact: Rutgers S. van der Hoeven
Cornell University
252 Emerson Hall, Ithaca, NY 14850, USA
Tel: 607 255 7886
Fax: 607 255 6683
Email: rv19@cornell.edu

FEATURES

source

Location/Qualifiers
1. 274

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="E6203"

/db_xref="taxon:4081"

/clone="cc-est1cbl18A13a1"

/tissue_type="developing flower buds and open flowers"

/dev_stage="4-8 week old plants"

/lab_host="XLOLR"

/clone_lib="Tomato flower library from a mixture of
developmental stages"

/note="Vector: pBK_CMY; Site_1: EcoRI; Site_2: XhoI;
flowers and flower buds were collected from greenhouse
grown plants and used for library construction (cbl)."

BASE COUNT 54 a 74 c 87 g 59 t

ORIGIN

Query Match

Best Local Similarity 59.1%; Pred. No. 5, 2e-15;

Matches 156; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 447 ATTGAGTGGGTCAGTTCGGAATGAGAGCGGCGGTTTGCAGCGGTGCGGAATCG 506

Db 264 ATCGAGTGGATGTCACCGCGGAGAGAGGCGGCGCTTGGCGGCGTGAACCA 205

QY 507 TTGATCACTGGGGAGCTGCGCATATGCTGCTTTTGTGTCGGAACACACCTG 566

Db 204 CACCTTAGGCGGAACCTGCGCGGCGGATGTCGCGGCGGCGGCGGCGGCGGACTTA 145

QY 567 ATTGAGGCTTTATGATTCGATGGAATGATGATGATGATGATGATGATGATGAT 626

Db 144 ATCAAGGCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 85

QY 627 ATTCGAGTGGCGCAATGTTGTCGACGTTTCCAGGAACGATCGGAGATTGTTT 686

Db 84 ATTCCTCCAGCGGAATGCGACGCGCTATTTCAGGAACCCACAGAGACTATTC 25

QY 687 AAGGATGCTCTGTTACTGCGAG 710

Db 24 CCGGATGTAGTCACTATTGCGAG 1

RESULT 11
BM534496/c 550 bp mRNA linear EST 19-FEB-2002
LOCUS
DEFINITION
IMAGE:5617763.5, similar to SW:POXB_ECOLI P07003 PYROVATE
DEHYDROGENASE; mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BM534496
EST.
Danio rerio (zebrafish)
Danio rerio

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 550)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood

TITLE
JOURNAL
COMMENT

Unpublished
Other ESTs: fw89h06.x1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: zbratish@wustl.edu
The library was constructed by Dr. Z. Gong. DNA sequencing by:
Washington University Genome Sequencing Center St. Louis. Please
contact Zhiyuan Gong for further information on this library
(National University of Singapore, Department of Biological
Sciences, Lower Kent Ridge Road, Singapore 119260).
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: T3 ET from Amersham
High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers
1. 550

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="IMAGE:5617763"

/sex="female"

/dev_stage="4-5 month"

/lab_host="DH10B (phage-resistant)"

/clone_lib="Gong zebrafish ovary"

/note="Organ: ovary (pooled); Vector: pluescript SK-
Site_1: XhoI; Site_2: EcoRI; Poly A+ RNA was isolated from
the ovaries of 2 female adult zebrafish (4-5 month old).
cDNAs were made using oligo-dT primers and inserted into
lambda zap II vector (Stratagene) by Dr. Z. Gong, in vivo
mass excised to pluescript SK- following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Zhiyuan Gong for further information on
this library (National University of Singapore,
Department of Biological Sciences, Lower Kent Ridge Road,
Singapore 119260)."

BASE COUNT 134 a 161 c 132 g 123 t

ORIGIN

Query Match

Best Local Similarity 4.2%; Score 89.8; DB 12; Length 550;

Matches 202; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

QY 447 ATTGAGTGGGTCAGTTCGGAATGAGAGCGGCGGTTTGCAGCGGTGCGGAATCG 506

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QY 507 TTGATCACTGGGGAGCTGCGCATATGCTGCTTTTGTGTCGGAACACACCTG 566

Db 376 CAGGATAGGCGGAGATGTCGCGGATATGATGATGATGATGATGATGATGATGAT 317

QY 567 ATTGAGGCTTTATGATTCGATGGAATGATGATGATGATGATGATGATGATGAT 626

Db 316 ATCAAGGCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 257

QY 627 ATTCGAGTGGCGCAATGTTGTCGACGTTTCCAGGAACGATCGGAGATTGTTT 686

Db 256 ATTCCTCCAGCGGAATGCGACGCGCTATTTCAGGAACCCACAGAGACTATTC 197

QY 687 AAGGATGCTCTGTTACTGCGAG 710

Db 196 CCGGATGTAGTCACTATTGCGAG 1

QY 747 CACGACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 806

Db 136 GCGATTGCCATGCCAAAGCGGTTCTATCTGTGGCGTTGCGTGTCTTACAGGC 77
 QY 807 GATATGCTAAGAGAACAGCGAGTGACG 835
 Db 76 GAAGTGGCGTTAAACCTGCGCCAGAG 48

RESULT 12
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 LOCUS B2549561 769 bp DNA linear GSS 17-DEC-2002
 DEFINITION pacsl-60_2172.xl pacsl-60 Pseudomonas aeruginosa genomic clone
 ACCESSION B2549561
 VERSION B2549561.1 GI:27153142
 KEYWORDS GSS.
 SOURCE Pseudomonas aeruginosa
 ORGANISM Pseudomonas aeruginosa
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

REFERENCE 1 (bases 1 to 769)
 Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
 Burns,J.L., Kaul,R. and Olsen,M.V.
 Whole-Genome-Sequence variation among multiple isolates of
 Pseudomonas aeruginosa library
 J. Bacteriol., (2002) in press
 CONTACT: Chris K. Raymond
 Genome Center
 University of Washington
 Box 352145, Seattle, WA 98105-2145, USA
 Tel: 2062216954
 Fax: 2066857244
 Email: ckraymond@u.washington.edu
 Class: shotgun.
 Location/Qualifiers
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 /organism="Pseudomonas aeruginosa"
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 /strain="1-60"
 /db_xref="taxon:287"
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BASE COUNT 112 a 241 c 280 g 134 t 2 others
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 Best Local Similarity 49.2%; Pred. No. 1,2e-13;
 Matches 285; Conservative 0; Mismatches 288; Indels 6; Gaps 2;

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 QY 583 ATTGCATGCAAAATGCTGGAGAGTGTGGCCATGCTTACCATTTCCGAGTCCCA 642
 Db 539 AGGCCAGCGCAACCGCGCCGATGCTGATCCAGCAGATCTTACCCGCAAC 480
 QY 643 TTGTGACGCTCTTCCAGAAACGATCCGAGATTTTGTTAAGATGCTGCTGT 702
 Db 479 TGGCAGTGAAGTTTCCCGAGAGAGTGATCTCAAGCGGCTTACGCGACCTGCTG 420
 QY 703 ACTGCAGATGTAATGTGTGTGACAGAGGTGAACGATTTTGCATCAGCGGATCA 762
 Db 419 TCTGCGAGCAGGTGCGACAGCCCGCAAGAGCGCGGCTGTGGCCCTGGCCTGCA 360
 QY 763 CCACATGCGGGGTAAAGTGTGGTGTGAGTGTGATGTTCTGTTGATGCTAAGAG 822
 Db 359 CGGGCTCAACCGCGCGGCTGTGGGTGTGATCTGCGCGCGCATC---ACCGAG 304
 QY 823 ACGAGGTGAGCTACTTATTTCAATTCACATTTCTGTGACATCTCTGTGTGTTC 882
 Db 303 GCCACGGTGAAGAGACCTGCGGTTCTGCTGATCTTCCCGCAACCGGTGCTGCGCCC 244

QY 883 CGGATCTACTGAGGCTGCCAGCGCTGTGGAGGCGATTAAACCGTAAGCTGTCACTT 942
 Db 243 AGCGAGCGGAACTGACAGAGCTGCGCCGCTGC--TGCCAGCGCAAGATTCGCA 186
 QY 943 TGTTCGCGTGCAGCGCTGGAAGATGCTCGCGCGCAAGTGTGAGTTGGCGGAGA 1002
 Db 185 TCTACGCGGCGGCTGCGCGTCCAGAGCGCGCAAGAGCTGTGTGTGCTGCGCCAGCGCC 126
 QY 1003 TTAATACCGATCGGCGATGCGCTGTGTGTGTAACGATACATCCAGTATGATCCGT 1062
 Db 125 TCAAGCGCCCGATCCCGCACACAGCTGCGCGACCAAGAGACTGTGTGATGACAAACCCCT 66
 QY 1063 TTGAGTGGCATGCTGTGCTGTGTGTGATGAGGCGCT 1101
 Db 65 TCAACATGGCGCATGCGCGTATGCTGCGAGGAGATCTT 27

RESULT 13
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 LOCUS B2571612 830 bp DNA linear GSS 17-DEC-2002
 DEFINITION msh2.1969.xl msh Pseudomonas aeruginosa genomic clone msh2.1969,
 genomic survey sequence.
 ACCESSION B2571612
 VERSION B2571612.1 GI:27206673
 KEYWORDS GSS.
 SOURCE Pseudomonas aeruginosa
 ORGANISM Pseudomonas aeruginosa
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

REFERENCE 1 (bases 1 to 830)
 Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
 Burns,J.L., Kaul,R. and Olsen,M.V.
 Whole-Genome-Sequence variation among multiple isolates of
 Pseudomonas aeruginosa library
 J. Bacteriol., (2002) in press
 CONTACT: Chris K. Raymond
 Genome Center
 University of Washington
 Box 352145, Seattle, WA 98105-2145, USA
 Tel: 2062216954
 Fax: 2066857244
 Email: ckraymond@u.washington.edu
 Class: shotgun.
 Location/Qualifiers
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 /strain="msh"
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 /note="Environmental isolate. Whole genomic shotgun library."

BASE COUNT 175 a 271 c 232 g 151 t 1 others
 ORIGIN

Query Match 3.9%; Score 85.2; DB 29; Length 830;
 Best Local Similarity 54.3%; Pred. No. 5.3e-13;
 Matches 171; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY 341 GCGAAGACATTAATTTGACATCTTGAAGCTCAAGGTGGAAGCGAATTTATGTTTGT 400
 Db 432 CGCGAGATCGTGTGGAACCTGTGAAGCGAGCGGTGCGCATCTGCTATGCGATGCT 491
 QY 401 GGGTACAGCTTATTCGATGCTGATGCTGTGCTGCGCAATACGATATGAGTGTCA 460
 Db 492 CGGCGACACCCATCAACCATGTTCACGAGCCATCATGCGACCGAGATCGATGAGTCA 551
 QY 461 CTTGGAATAGAGAGAGCGCGGCTTGTGACAGCGCGTGGGAATGCTGATCAGTGGGA 520
 Db 552 CGTGGCGACAGAGAGAGCGGTGAGTGTGCGCGGCGCGAGTGTCTACATTAAGGAGCG 611

Tue Oct 7 07:11:16 2003

us-09-965-825-1.rst

Page 10

Search completed: October 3, 2003, 18:49:55
Job time : 4101 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 3, 2003, 17:41:32 : Search time 541 Seconds

(without alignments)
10184.593 Million cell updates/sec

Title: US-09-965-825-1

Sequence score: 2160
1 tagagcgatctgtgaggg.....ggtgccatgattgacct 2160

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1708419 seqs, 1275431651 residues

Total number of hits satisfying chosen parameters: 3416838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2160	100.0	2160	US-09-965-825-1	Sequence 1, Appli
2	2160	100.0	2160	US-10-336-049-4	Sequence 4, Appli
3	2160	100.0	2160	US-10-143-856-3	Sequence 3, Appli
4	2160	100.0	2160	US-10-078-167-6	Sequence 4, Appli
5	2160	100.0	3248	US-09-965-825-4	Sequence 4, Appli
6	2160	100.0	3309400	US-09-738-626-1	Sequence 1, Appli
7	1737	80.4	1737	US-09-738-626-2873	Sequence 2873, Ap
8	875	40.5	875	US-09-965-825-7	Sequence 3, Appli
9	875	40.5	875	US-10-336-049-6	Sequence 6, Appli
10	875	40.5	875	US-10-143-856-5	Sequence 5, Appli
11	875	40.5	875	US-10-078-167-6	Sequence 6, Appli
12	523	24.2	9025608	US-10-156-761-1	Sequence 1, Appli
13	522.6	24.2	1740	US-10-156-761-2067	Sequence 2067, Ap
14	344.8	16.0	1719	US-09-815-242-9898	Sequence 9898, Ap
15	324.4	15.0	1422	US-09-965-825-12	Sequence 12, Appli
16	305.2	14.1	1719	US-09-815-242-6012	Sequence 6012, Ap

17	305.2	14.1	1719	13	US-10-096-571-1	Sequence 1, Appli
18	209	9.7	1140	10	US-09-738-626-2872	Sequence 2872, Ap
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20	206	9.5	1761	14	US-10-096-571-943	Sequence 943, Appli
21	155	7.2	1454	13	US-10-096-571-7	Sequence 7, Appli
22	152.8	7.1	1448	13	US-10-096-571-8	Sequence 8, Appli
23	139.4	6.5	1737	9	US-09-815-242-4766	Sequence 4766, Ap
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29	79.2	3.7	589	9	US-09-815-242-1850	Sequence 2854, Ap
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31	68.8	3.2	2111	13	US-10-096-571-11	Sequence 13, Appli
32	68.8	3.2	2111	13	US-10-096-571-13	Sequence 11, Appli
33	68.8	3.2	2111	14	US-10-096-595B-11	Sequence 13, Appli
34	68.8	3.2	2111	14	US-10-096-595B-13	Sequence 9337, Ap
35	67.4	3.1	1647	9	US-09-815-242-9337	Sequence 6310, Ap
36	62.4	2.9	984	9	US-09-815-242-6310	Sequence 9527, Ap
37	59.8	2.8	1776	9	US-09-815-242-9527	Sequence 35, Appli
38	57.2	2.6	1968	11	US-09-887-194A-35	Sequence 42, Appli
39	56.8	2.6	2702	9	US-09-732-618-42	Sequence 2720, Ap
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41	54.8	2.5	1848	14	US-10-156-761-2720	Sequence 1, Appli
42	53.4	2.5	3390	10	US-09-767-878-1	Sequence 481, Ap
43	52.8	2.4	1503	10	US-09-974-300-481	Sequence 493, Ap
44	52.8	2.4	1539	10	US-09-974-300-493	Sequence 9, Appli
45	51.2	2.4	990	12	US-10-307-138-9	

ALIGNMENTS

RESULT 1
US-09-965-825-1
Sequence 1, Application US/09965825
Patent No. US2002015099A1
GENERAL INFORMATION:
APPLICANT: DUSCH, Nicole
APPLICANT: THOMAS, Hermann
APPLICANT: THERBACH, Georg
TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENIC AC
FILE REFERENCE: 2135405X
CURRENT APPLICATION NUMBER: US/09/965, 825
PRIOR FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: DE 10048604.5
PRIOR FILING DATE: 2000-09-30
PRIOR APPLICATION NUMBER: DE 10117085.8
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2160
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: CDS
LOCATION: (327)..(2063)
OTHER INFORMATION:
NAME/KEY: -35 signal
LOCATION: (227)..(232)
OTHER INFORMATION:
NAME/KEY: -10 signal
LOCATION: (256)..(261)
OTHER INFORMATION:
US-09-965-825-1

Query Match 100.0%; Score 2160; DB 10; Length 2160;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1621 CGATGCTGTGAGAGGAGACGCGGATTTGGGATGCTGCTGGTGGATCTGACCGTTAGCT 1680
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OY 1861 AGCAGTACCTGAGGATGGCATATCCGAGACCTGTACTGATCATATCTGACGATC 1920
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OY 1921 CTAATGCTGTGATCCCAACCAATCAGTGGGAACAGGTCAATGGGATTCAGCAAG 1980
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OY 1981 CGGCGACCGGAACCGCTTTGTGTGAGAGGTGAGAGCATATGATGATGCGCGGTG 2040
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Db 2101 GCGCTTAATGCGCAATTTCCAGATGAGAGTGCACCGCGGTGCGCATGAGATG 2160

RESULT 2

US-10-336-049-4
; Sequence 4, Application US/10336049
; Publication No. US2003017591A1
; GENERAL INFORMATION:
; APPLICANT: Hans, Stephan
; APPLICANT: Bath, Brigitte
; APPLICANT: Beth, Alexander
; APPLICANT: Thierbach, George
; APPLICANT: Kreutzer, Caroline
; APPLICANT: Mockel, Bettina
; TITLE OF INVENTION: Process for the Preparation of L-Amino Acids with Amplification
; TITLE OF INVENTION: The zwf Gene
; FILE REFERENCE: 7601/80158
; CURRENT APPLICATION NUMBER: US/10/336,049
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 2160
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (327)..(2063)
; OTHER INFORMATION: poxb
US-10-336-049-4

Query Match 100.0%; Score 2160; DB 12; Length 2160;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGAGGCGATTCGTGAGAGTCACTTTTGGGGTGGGGTCTAATTTGGCCAGTTT 60
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DB 61 CGAGGCGACAGACAGCGCGCCACGATGTTAAATAGCGATGGGCGCATCTGT 120
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DB 541 CTTTGGTCTCTGGAACACACACCTGATTCAGGCTTTATATTCGCAATGCTG 600
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RESULT 4
US-10-078-167-4

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; Sequence 4, Application US/10078167
; Publication No. US20030119154A1
; GENERAL INFORMATION:
; APPLICANT: Danicam, Rita
; APPLICANT: McCormack, Ashling
; APPLICANT: Stapleton, Cliona
; APPLICANT: Burke, Kevin
; APPLICANT: Mockel, Bettina

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; TITLE OF INVENTION: Process for the preparation of L-amino acids using
; FILE REFERENCE: 990229 BT-US-B
; CURRENT APPLICATION NUMBER: US/10/078.167
; CURRENT FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2160
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (327)..(2063)
; OTHER INFORMATION: poxb
US-10-078-167-4

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Query Match 100.0%; Score 2160; DB 14; Length 2160;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 781 GTGTGTGCTGAGTATGATTCCTGATATCCGTAAGAGACGAGTGACGATCTT 840
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QY 1681 ACCAACTTCCGCTGAAGAGTGTGTTTAAACAAGTCTTGGGATGATGATGATG 1740
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QY 1741 AGATGCTGTGAGAGGACAGCAGAAATTTGATCTAGTACCATGAGAGAGTGAATTTGCGAG 1800
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QY 1801 AGATGCTGTGAGAGGACAGCAGAAATTTGATCTAGTACCATGAGAGAGTGAATTTGCGAG 1860
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DB 1861 AGCAGCTAGCTGAGGACATTCCTGAGACCTGATGATGATGATGATGATGATGATGATG 1920

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DB 2041 ACATAAGAAATATTCCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2100
QY 2101 GGGCTTAATGCTGACATTTCCAGATGAGGACCTACGCGGCTGCCATGAGATGCGCT 2160
DB 2101 GGGCTTAATGCTGACATTTCCAGATGAGGACCTACGCGGCTGCCATGAGATGCGCT 2160

RESULT 5
US-09-965-825-4
; Sequence 4, Application US/09965825
; Patent No. US2002015099A1
; GENERAL INFORMATION:
; APPLICANT: DUSCH, Nicole
; APPLICANT: THOMAS, Hermann
; APPLICANT: THIERBACH, Georg
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENIC ACID
; FILE REFERENCE: 2134US0X
; CURRENT APPLICATION NUMBER: US/09/965, 825
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: DE 10048604.5
; PRIOR FILING DATE: 2000-09-30
; PRIOR APPLICATION NUMBER: DE 10117085.8
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 3248
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (802)..(2538)
; OTHER INFORMATION:
US-09-965-825-4

Query Match 100.0%; Score 2160; DB 10; Length 3248;
Best local similarity 100.0%; Pred. No. 0;
Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAGAGGCGATTCCTGTGAGTCACTTTTGTGGGCTCGGGGCTAAATTTGGCCAGTTT 60
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DB 241 AAGCGTGCAACACTGGAATTTAAGACACAAATTTGAAGTGCACCAAGTTAGGCAAC 300
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Db 1976 ACATGAGAAATCCGAGGAGAACCGGAGCTTTGTGGTTCTATTCGCCACAGGACGATG 2035
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Db 2036 CTAAATCGTTGCTCTATGCGATTTGGTCCGAAAGTGTGATCGAAACCGCAGGTATCG 2095
QY 1621 CGATGTGTGGCAGTGTGGTTGGGATGCTGTGGGTGAGCTTCTGACCGTTAACTGC 1680
|||||
Db 2096 CGATGTGTGGCAGTGTGGTTGGGATGCTGTGGGTGAGCTTCTGACCGTTAACTGC 2155
QY 1681 ACCAACTTCGCTGTAAGGCTGTGTGTTTAAACAACAGTTCTTTGGCATGTGAAGTGG 1740
|||||
Db 2156 ACCAACTTCGCTGTAAGGCTGTGTGTTTAAACAACAGTTCTTTGGCATGTGAAGTGG 2215
QY 1741 AGATGCTGTGAGAGGACACCGAGAAATTTGTGTAAGTACCATGAGAGTGAATTTGCGAG 1800
|||||
Db 2216 AGATGCTGTGAGAGGACACCGAGAAATTTGTGTAAGTACCATGAGAGTGAATTTGCGAG 2275
QY 1801 AGATTGGGCGGCTGTGGGTATCCAAATGCTGTGACCATGACCATCCGAGAAAGTTCGCG 1860
|||||
Db 2276 AGATTGGGCGGCTGTGGGTATCCAAATGCTGTGACCATGACCATCCGAGAAAGTTCGCG 2335
QY 1861 AGCACTAGCTAGGCAATGTCATATCCGAGACCTGTGATGATGATGATGATGATGATGATG 1920
|||||
Db 2336 AGCACTAGCTAGGCAATGTCATATCCGAGACCTGTGATGATGATGATGATGATGATGATG 2395
QY 1921 CTAAATGCTGTGATCCACCAACCATATGCTGTGGAGACAGTCAATGAGATTCAGCAAG 1980
|||||
Db 2396 CTAAATGCTGTGATCCACCAACCATATGCTGTGGAGACAGTCAATGAGATTCAGCAAG 2455
QY 1981 CGGCGCACCGAACCCTTTTGGTGTGAGAGTGTGAGAGCGATGATGATGATGATGATGATG 2040
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Db 2456 CGGCGCACCGAACCCTTTTGGTGTGAGAGTGTGAGAGCGATGATGATGATGATGATGATGATG 2515
QY 2041 ACATTAAGAAATATTTCTACTCATGATGATGATGATGATGATGATGATGATGATGATGATG 2100
|||||
Db 2516 ACATTAAGAAATATTTCTACTCATGATGATGATGATGATGATGATGATGATGATGATGATG 2575
QY 2101 GCGCTTACTGCGCAACATTTCCAGATGTGCGAGCTACGCGGCTGCCATGAGATTTGCCCT 2160
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Db 2576 GCGCTTACTGCGCAACATTTCCAGATGTGCGAGCTACGCGGCTGCCATGAGATTTGCCCT 2635
|||||

RESULT 6
US-09-738-626-1/c
: Sequence 1, Application US/09738626
: Publication No. US20020197605A1
: GENERAL INFORMATION:
: APPLICANT: NAKAGAWA, SATOSHI
: APPLICANT: MIZOGUCHI, HIROSHI
: APPLICANT: ANDO, SEIKO
: APPLICANT: HAYASHI, MIKIRO
: APPLICANT: OCHIAI, KEIKO
: APPLICANT: YOKOI, HARUHIKO
: APPLICANT: TATEISHI, NAOKO
: APPLICANT: SENOH, AKIHIRO
: APPLICANT: IKEDA, MASATO
: APPLICANT: OZAKI, AKIO
: TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
: FILE REFERENCE: 249-125
: CURRENT APPLICATION NUMBER: US/09/738, 626
: CURRENT FILING DATE: 2000-12-18
: PRIOR APPLICATION NUMBER: JP 99/377484
: PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 1
LENGTH: 3309400
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match 100.0%; Score 2160; DB 10; Length 3309400;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TTAGAGCGATCTCTGAGAGTCACTTTTGTGGGTCGGGGCTAAATTGGCCACTTTT 60
Db 2778830 TTAGAGCGATCTCTGAGAGTCACTTTTGTGGGTCGGGGCTAAATTGGCCACTTTT
QY 61 CGAGCGCAGCAGACAGGCGTCCCGCAGATGTTTAAATAGGCGATCGGTGGGCACTGTGT 120
Db 2778770 CGAGCGCAGCAGACAGGCGTCCCGCAGATGTTTAAATAGGCGATCGGTGGGCACTGTGT
QY 121 TTGGTTTCAGCGGGGCTGAACCAACACAGACTGCCAGCAGACAGAGGAAATCCCAAAAT 180
Db 2778710 TTGGTTTCAGCGGGGCTGAACCAACACAGACTGCCAGCAGACAGAGGAAATCCCAAAAT
QY 181 GGGCATCCCTGTTTGTGTAACGAGTACCCACCCGGGCTGAACCTCCCTGGCAGCGGGG 240
Db 2778650 GGGCATCCCTGTTTGTGTAACGAGTACCCACCCGGGCTGAACCTCCCTGGCAGCGGGG
QY 241 AAGCGTGGCAACAACAGTGAATTTAAGACACATTAAGTCGACCAAGTATAGGCAACAC 300
Db 2778590 AAGCGTGGCAACAACAGTGAATTTAAGACACATTAAGTCGACCAAGTATAGGCAACAC
QY 301 AATAGCCATACGTTGAGAGTTCAGATGCGACACAGCTACGACAGCAATTAATTAAGCA 360
Db 2778530 AATAGCCATACGTTGAGAGTTCAGATGCGACACAGCTACGACAGCAATTAATTAAGCA
QY 361 CTTTGGAGCTCAAGGTGTGAAGCAATTTATGTTTGGGTGACAGCTTAATCCGA 420
Db 2778470 CTTTGGAGCTCAAGGTGTGAAGCAATTTATGTTTGGGTGACAGCTTAATCCGA
QY 421 TCGTGATGCTTCGCCAATCAGATATTGAGTGGTGCACGTTCCAAATGAGAGACGG 480
Db 2778410 TCGTGATGCTTCGCCAATCAGATATTGAGTGGTGCACGTTCCAAATGAGAGACGG
QY 481 CGGCGTTTGCAGCGCGGTGCGGAATCGTGAATCACTGGGAGCTGGCAGTATGTGCTT 540
Db 2778350 CGGCGTTTGCAGCGCGGTGCGGAATCGTGAATCACTGGGAGCTGGCAGTATGTGCTT
QY 541 CTTGTGCTCTGGAACACACACCTGATTAGGGTCTTTATGATTGCAATCGAAATGTTG 600
Db 2778290 CTTGTGCTCTGGAACACACACCTGATTAGGGTCTTTATGATTGCAATCGAAATGTTG
QY 601 CGAAGGTGTTGGCCATCGCTAGCCATATTCGAGTCCGACCCAGATGGTTCACCTTCTTC 660
Db 2778230 CGAAGGTGTTGGCCATCGCTAGCCATATTCGAGTCCGACCCAGATGGTTCACCTTCTTC
QY 661 AGAAGACGATCCGAGATTTTGTAAAGATGCTGTGTTCTGCTGAGATGTTGAATG 720
Db 2778170 AGAAGACGATCCGAGATTTTGTAAAGATGCTGTGTTCTGCTGAGATGTTGAATG
QY 721 GTGGTGAAGAGGTGAACGCAATTTGCATACGCGATTCAGTCCACCATGGCGGTTAAAG 780
Db 2778110 GTGGTGAAGAGGTGAACGCAATTTGCATACGCGATTCAGTCCACCATGGCGGTTAAAG
QY 781 GTGTGCGGTGTAGTATCTGTGATATTCGCTAAGAGAGAGAGAGAGAGAGTACTT 840
Db 2778050 GTGTGCGGTGTAGTATCTGTGATATTCGCTAAGAGAGAGAGAGAGAGTACTT
QY 841 ATTCAATTCACATATTTCTTTCGCACTCTGTGTCTCCGAGATCCACTAGAGCTG 900
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Db 2777990 ATTCAATTCACATATTTCTTCTGCACTCTGTGTCTCCGAGATCCACTAGAGCTG 2777931
QY 901 CAGCGCTGTGAGGCGAATTAAACAGCTAGTCTGCTACTTTGTTTGGGTGGGCGG 960
Db 2777930 CAGCGCTGTGAGGCGAATTAAACAGCTAGTCTGCTACTTTGTTTGGGTGGGCGG
QY 961 TGAAGATGCTCGCGCAGAGGTGTGAGTGGCGGAGAAATTAATCAGCATCGGCG 1020
Db 2777870 TGAAGATGCTCGCGCAGAGGTGTGAGTGGCGGAGAAATTAATCAGCATCGGCG
QY 1021 ATGCGCTGGGTGTGAAGAGTATCATCAGCATGAGAAATCCGTTGAGTGGCATGTG 1080
Db 2777810 ATGCGCTGGGTGTGAAGAGTATCATCAGCATGAGAAATCCGTTGAGTGGCATGTG
QY 1081 GCCTGCTGTGTAGCGCGCTCGGAGTGGTCCAAATGAGGCGGATCGTGAATTCAT 1140
Db 2777750 GCCTGCTGTGTAGCGCGCTCGGAGTGGTCCAAATGAGGCGGATCGTGAATTCAT
QY 1141 TTGGTACGATTTCCCTTATTCGTGATTTCTCTCTAAAGACACGTTGCCAGTGTGATA 1200
Db 2777690 TTGGTACGATTTCCCTTATTCGTGATTTCTCTCTAAAGACACGTTGCCAGTGTGATA
QY 1201 TCAACGGTGGCAGATTTGGTGGAGTACCAAGGTAAGTACCGGTGAGTGTG 1260
Db 2777630 TCAACGGTGGCAGATTTGGTGGAGTACCAAGGTAAGTACCGGTGAGTGTG
QY 1261 CTGCAACAATCGAAATATTTTCTCTCATGTGAAGAAACACATGCTCTCTCTG 1320
Db 2777570 CTGCAACAATCGAAATATTTTCTCTCATGTGAAGAAACACATGCTCTCTCTG
QY 1321 ATCGATGCTCAAGGACACAGCGTAAAGTACGCTGGTGTAAAGAGTACACATA 1380
Db 2777510 ATCGATGCTCAAGGACACAGCGTAAAGTACGCTGGTGTAAAGAGTACACATA
QY 1381 ACGTGAGAGCATGTGCTATTCACCCGATAGCTTCCCTATTTTGAAGAGCTG 1440
Db 2777450 ACGTGAGAGCATGTGCTATTCACCCGATAGCTTCCCTATTTTGAAGAGCTG
QY 1441 CGGATTAAGATCGGTGTTTACTGTGATACCGCATGCGCATGTGCGATGCGAGGT 1500
Db 2777390 CGGATTAAGATCGGTGTTTACTGTGATACCGCATGCGCATGTGCGATGCGAGGT
QY 1501 ACATGAGATCGGAGGGAACGCGCATTTGTGGTTCATTCGCCACGACAGATG 1560
Db 2777330 ACATGAGATCGGAGGGAACGCGCATTTGTGGTTCATTCGCCACGACAGATG
QY 1561 CTAATGCTGCTCATGCGATGTGTCGCAAAAGTGTGATGAAACCCGACAGTGTG 1620
Db 2777270 CTAATGCTGCTCATGCGATGTGTCGCAAAAGTGTGATGAAACCCGACAGTGTG
QY 1621 CGATGCTGCGATGGTGTGTTGGCATGCTGCTGGTGAAGTTCGACCCGTTAAGCTG 1680
Db 2777210 CGATGCTGCGATGGTGTGTTGGCATGCTGCTGGTGAAGTTCGACCCGTTAAGCTG
QY 1681 ACCAATTCGCTGAAGGCTGTGTTTAAACACAGTTCTTTGGGCAATGGGAAGTTG 1740
Db 2777150 ACCAATTCGCTGAAGGCTGTGTTTAAACACAGTTCTTTGGGCAATGGGAAGTTG
QY 1741 ACATGCTGTGAGGAGCAGCCAGATTTGTAGTACCATAGGAAGTGAATTCGAG 1800
Db 2777090 ACATGCTGTGAGGAGCAGCCAGATTTGTAGTACCATAGGAAGTGAATTCGAG
QY 1801 AGATTGCGGCTCGGGTATCAATGCGTACGATACCGATCCGAAGAAAGTTCGCG 1860
Db 2777030 AGATTGCGGCTCGGGTATCAATGCGTACGATACCGATCCGAAGAAAGTTCGCG
QY 1861 ACAGCTACTAGGCAATTTGCGATTCCTGACCTGTACTGATGATATGCTACAGATC 1920
Db 2776970 ACAGCTACTAGGCAATTTGCGATTCCTGACCTGTACTGATGATATGCTACAGATC
QY 1921 CTAATGCTGCTGCAACCCACCAACATCAGCTGGAACAGTTCATGGATTCACAGG 1980
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Dh 2532155 CCCCTCCAGGAGATCGGCCTCGCATTTCTTCCAGAGAACCCATCCGACAGCTTTCCG 2532096
QY 689 GGAATGCTCTGGTACTGCGAGATGTTGAATGGTGGAGCAGGGTCAACGCATTTTGTGA 748
Db 2532095 CGAGTGCATCTACTACGAGGATGATCTCCAAACCCGAAACGATGCGGAGCTGTGCA 2532036
QY 749 TCACGGATTTCATCCACCATGGCGGGTAAAGGTGTGTGGTGTGTGATTTCTGTGA 808
Db 2532035 GTCCGCGATTCAGACACCGCGTGGTCAATCCGCTCAAGCTGTCAACCTCCCGCGA 2531976
QY 809 TATCGCTAAGAGAGACGAGTGCAGCTACTTATTCCAATTCCTACTATTTCTGTGAC 868
Db 2531975 CGTCGCTCCGAGACCGCCCGGACAAAGCGCTCGAGAACCGCCCTGTGACCTCCGCGC 2531916
QY 869 TCCCTGTGTGTTCCCGGATCTCTACTAGCTGCAGCGCTGTGTGAGGCGATTAAACGC 928
Db 2531915 CACGGTCCGCGCCCGGGA--CACCGAGATCGCAAGCTCTGTCGCTTGTATCGACGCGC 2531859
QY 929 TAAGTGTCTACTTTGTGTGGCGTGCGGCGGTGAAGAAATGCTCGCGCGAGGTGTGGA 988
Db 2531858 CGACAAAGTCAACCTCTTTGTGGCGAGCGGCGACGCGGCGGTGCGACGCGAGGTCAATGA 2531799
QY 989 GTTGGCGGAGAAATTAATCAACCGATCGGGCATGCGGTGGGTGTAAAGCATATCA 1048
Db 2531798 GTTCCGCCGAGAAATCAATGTCCTCCGCGTCCGCGACGCGGTGGCGGCAAGAGTGTATCA 2531739
QY 1049 GCATGAGATCCGTTTGAAGTGGGATGTCTGCGCTGCTGTGTTACGCGCCTGCGTGA 1108
Db 2531738 GTACGACAAACCGCTACGAGTGGCGATGAGCGGCTCTCGGCTACGCTGCCCTACGA 2531679
QY 1109 TCGTCCAAATGAGCGGATCTCTGTATTTGATGAGTATTCCTTATTTCTATTT 1168
Db 2531678 GGCACACAAACGATGGATCTGTATCTGTCTGCTGCGACCGACTTCCGTTACACGCTT 2531619
QY 1169 CCTTCTTA--AAGAACACGTTGCCAGGTGATATCAACGCTGCACATGTGTGACG 1225
Db 2531618 CTTCCCAACCGATGGAATGACAGAGTTCAGACGTCGCGCCCGGAACGCTGCGCGG 2531559
QY 1226 TACCAAGGTGAGTATCCGCTGACCGGTATATGTGTGCAACAAATCGAAATTTTGGC 1285
Db 2531558 CTCGAAGTTGACCTGCGCTGTGGGCGATGTGGGAGACCTTCGCTGTATCC 2531499
QY 1286 TCATGTGAAGAAAAACAGATCTTCTTCTTATGCGATGTCTCAACGACGACGAGG 1345
Db 2531498 GCGGGTGAAGCCCAAGAGAACCGCGGCTCTCCGACAAAGATGCTGAGAAAGCAGCGGA 2531439
QY 1346 TAAATTGAGCTGGGTGAGACGTAACATTAACCTCGAAGAACATGTCTCAATTTCA 1405
Db 2531438 CGCGCTGGAAGGTGTTCATCAAGGCGTACACGCGAAGGTGAGAAAGCAGTCCGATCA 2531379
QY 1406 CCTGTAATACGTTGCTCTATTTTGAAGAGCTGGCGGATTAAGGATGCGGTCTTACTGT 1465
Db 2531378 CCGCGAGTACGTGGCTCTCGCTCTCGACGAACTGGCCGCGGAGACGCGGTTCACCGT 2531319
QY 1466 GGAATACCGGATGTCAATGTGTGCAATCGAGTACATCGAATTCGAGAGGACGCG 1525
Db 2531318 CGACACCGGATGTCAATGTGTGCGGCGCGCTACATCTCTG---CCCAAGGACGCGC 2531262
QY 1526 CGACTTTGTGGTTCATTCGCGACGCGACGATGCTTAATGCGTTCATGCGATTTGG 1585
Db 2531261 CCGGCTCAATGCGCTGTCTGCGACGCTCCATGCGAAGCGGCTGCGGATGGCATGG 2531202
QY 1586 TCGCAAAAGTGTTCGAAACCGCGAGGTGATGCGGATGCGGATGCGGTGTTGG 1645
Db 2531201 CGCCAGATTCAACGACGCGAAACCGGAGGTCTCTCGATGTGCGGAGCGGAGTTCGC 2531142
QY 1646 CATGCTGCTGGGTGAGCTTCTGACGTTAAGCTGCACCAACTTCGCTGGAAGGCTGTGT 1705
Db 2531141 CATGCTGATGGGCACTCTCTCACCTCGTCCAGTACACGTGCCGGTGAAGTGTGACT 2531082
QY 1706 GTTTAAACAGAGTCTTTGGGCAATGTGAAGTGTGAGTGTGCGTGTGAAGGACACGACGA 1765
Db 2531081 GTTCAACAACTCTCTTGTGACATGTGAGTGTGAGTGTGCGCGGCGCTCTC 2531022

QY 1766 ATTTGTACTGACCATGAGGAGTGAATTTCCGAGAGATTCCGCGCTGCGGTATCA 1825
Db 2531021 GTACGGACACCAAGAAAGAACCCGACTTCCGCGCGTCCGACAGAGCTGTGGCGCTA 2530962
QY 1826 ATCGGTACGATCACCATCCGAAGAAAGTTCCGACAGCTAGCTAGGCAATTGGCATA 1885
Db 2530961 CCGGCTGCGGGTGCAGAAAGCCCAAGCAACTCGCGGGCGCTGAAGACGCTTCAGGA 2530902
QY 1886 TCCGTGACCTGTACTGATTCATATTCGACAGGATCTTAATGCGCTGTGATCCACCAAC 1945
Db 2530901 CAAGGACCGGCTCTGTCAATCTGTGACCGACCCCAACGCTGTCAACCGCGGA 2530842
QY 1946 CATCACGTGGAAACAGGTCAATGGGATTACGAAGCGGCGCAACCGGACCTTTGGTGG 2005
Db 2530841 GATCAGCGGGAAGTGTGAAGGCGCTTCCGCGTCTCGGAAGTGTGTCTGTGACG 2530782
QY 2006 AGGAGTATGAGAGCATGATTCATCTGCGCCGTTGCAACATAAGAAATATTCCTACTCAT 2064
Db 2530781 CCGGCTGCGCGGATGTGTGATGATGCTGCCCTCCAACTGCGAAGCTGCGCGCTCTT 2530723

RESULT 13

US-10-156-761-2067
; Sequence 2067, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2067
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1740)
US-10-156-761-2067

Query Match 24.2%; Score 522.6; DB 14; Length 1740;
Best Local Similarity 57.9%; Pred. No. 4.5e-161;

Matches 1006; Conservative 0; Mismatches 719; Indels 12; Gaps 4;

QY 332 ACACAGCTACGAGAAATTAATGACATTTGGAAGCTCAAGGTGTGAAGGAATTTA 391
Db 9 ACAGAAACGTCGCGAGCAATTTGTGCAATCTCTCCGCGGCGGTCAATGCTGTGA 68
QY 392 TGGTTTGTGGGTGACAGCTTAAATCGATCGTGTGATGCTGTCCGCC---AATCAGATAT 448
Db 69 CCGGGGTGGGTGACAGTCTCAACCCGCTGTCGACGCAATTCGCGCAACTCCGCAT 128
QY 449 TGAGTGGGTGACGTTTCGAAATGAGGAACCGCGGCTTTGACGCGGTGGGAATGCTT 508
Db 129 CGACTGTGATTCAGTCGCGACAGAGGGAACCGCGCTTTCGCGCGGCGGAGGCGGA 188
QY 509 GATCACTGGGAGCTGCGAGTATGTGCTCTTGTGTGCTCTGGAACACACACACTGTAT 568
Db 189 GATCACCGGCAAGTCTGCGCGCTGCGCGCTCTGTGCGGCCCGGGAACCTCAGCTCAT 248
QY 569 TCAGGCTCTTTATGATTCGATCGAAATGTGTGCGAAGGTGTTGGCCATGCTAGGCATAT 628

Db 249 CAAGGCGCTGTACGACGGCCACCGCTCCATGGCGCGGCTCCGCGCTCGCTCGCACAT 308
Qy 629 TCCGAGTCCCGCAGATGGTTGACGTTCTTCCAGAAAACGATCCGAGATTTGTTAA 688
Db 309 CCCCCTCAGCGAGATCGGCTCGATCTTCTCCAGAGACCCATCCCGACACACTCTTCGG 368
Qy 689 GGAATGCTGTGGTCTGCTGAGATGGTGAATGGTGTGAGCAAGGGTGAACGATTTTGA 748
Db 369 CGAGTGCAGTCACTACAGCGAGATGATCTCCAAACCGAAGAGATGCCGAGGCTCTGCA 428
Qy 749 TCAGCGATTCATCCACCATGCGCGGTAAGGTGTGTGGTGTGAGTATGATTCCTGGTGA 808
Db 429 GTCCGCCATTCAGACACGGCGGTGGGTCACTCCGGCGCTCAGCGCTCGACCTCCCGGGA 488
Qy 809 TATGCTTAAAGAAACGAGTGAACGCTGATCTTATTCATTCATTCATTTCTTGTGAC 868
Db 489 CGTGCGCTCCAGCGCGCGCGCGCGGACAAAGCGCGTGAAGACCCCTCTGTACCTCCGGCC 548
Qy 869 TCCTGTGGTGTTCGCGATCTCTAGAGGCTGACAGCGCTGTGGAGGGGATTAACACGC 928
Db 549 CACGCTCCGCGCGCGCGCAGC---ACCGAGATGACAAAGCTCTCGGTTGATCGACGCGC 605
Qy 929 TAACTCTGTCACTTGTGTCGGTTCGCGGCGGTGAAGATGCTCGCGCGAGTGTGGA 988
Db 606 CGACAGGTCACCCCTCTTCTCGCGGACGCGGACGCGGCGGTGCGACGCGGATGATGA 665
Qy 989 GTTGGCGAGAAATTAATCAGCATCGCGGATCGCGTGGTGTAAAGCATATCA 1048
Db 666 GTTGGCGAGAAATTAATCAGCATCGCGGATCGCGTGGTGTAAAGCATATCA 1048
Qy 1049 GCATGAGAAATCCGTTTGAAGTGGCATGTGCGCGCTGTTGTTACGCGCGCTGCTGGA 1108
Db 726 GTAGACAAACCCGTCAGCGCGTGGCATGAGCGGCTCTCGGCTACGCTGCGCGCTACGA 785
Qy 1109 TGGCTCCAATGAGCGGATCTGCTGATTTCTATTGGGTACGAGATTCCTTATTCGATTT 1168
Db 786 GGGCACCACAGAGTGCATCTGCTGATCTGCTGCGGACCGACTTCCGTTCAACAGCTT 845
Qy 1169 CTTTCTTA---AAGACAAAGTGTGCGGAGTGGATATCAAGGTGCGGACATGTGTCAGC 1225
Db 846 CTTTCTTA---AAGACAAAGTGTGCGGAGTGGATATCAAGGTGCGGACATGTGTCAGC 1225
Qy 1226 TACCAGGTGAAGTATCCGCTGACCGGTGATGTTGTCGAACAATTCGAAATATTTGGC 1285
Db 906 CTGGAAGTGGACCTCCCTCTGCGGCGATGTGCGGAGACCTCGGCTGTGATGCC 965
Qy 1286 TCATGTAAGGAAAAACAGATGTTCTTCTTCTGATCGATGCTCAAGCAGCAGCG 1345
Db 966 GCGGCTGAAGCCCAAGAGAACCGCGCTTCTCGAACAAGATGCTGAAGAACGCGGA 1025
Qy 1346 TAACTGAGCTCGGTGTAGAGAGTACACATTAACGTGAGAGATGCTTCA 1405
Db 1026 CCGGCTGAAGGTGTATCAAGGGGTACAGCGGAGAGTGTGAGAGACGTTCCGATCCA 1085
Qy 1406 CCGTGAATAGTTCCTCTATTGTTGAACGAGTGGCGGATAGAGATCGGTTTACTGT 1465
Db 1086 CCGGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1145
Qy 1466 GATATCCGCGATGTCGAATGTGTGGATGGAGGTGATGTCGAGTATCCGAGGAGCGC 1525
Db 1146 CGACACCGGATGTGCAATGTCTGCGGCGCGCGCTCTCATCTG---CCCAACGAGCGCG 1202
Qy 1526 CGACTTGTGGGTTCAATCCGCGACGCGAGATGGCTAAATGCTTCTCATCGATGG 1585
Db 1203 CCGGCTGATCAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1262
Qy 1586 TGGGCAAGTGTGATCGAAACCGCAGGATGCGGATGTGGCGATGTGGG 1645
Db 1263 CCGCCGTTTACCGGACCGGAGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1322
Qy 1646 CAGTCTGTGGTGAAGCTTCTGACCTTAAGCTGACCAACTTCCCTGAAGGCTGTGG 1705

Db 1323 CATGCTGATGGCGACTTCTCTACCTCTGTCCAGTACGACTGCCGTTGAAGTGTACT 1382
Qy 1706 GTTAAACAACAGTCTCTTTGGCATGGTGAAGTTGAGATGCTGCTGAGGAGCAGCAGA 1765
Db 1383 GTTCAACAACCTCTCTTGTAGCATGTGCAAGTTGAGATGTGTGGTGGCGGCTGCTTC 1442
Qy 1766 ATTTGGTACTGACCATGAGGAAGTAAATTTGCGAGAGATTTGGCGGCTGCGGATCAA 1825
Db 1443 GTACGCGACACAGAACCAAGACCCGACTTCCGCGCGCTGCGAGAGCTGTGGGCGTA 1502
Qy 1826 ATCGGTAGCATCACCAGATCCGAAAGATTTGCGAGCGCTAAGCTGAGGCAATGCAATA 1885
Db 1503 CGGCTGTGGGCTGAGAAACCCAGCAACTCCGCGCGCTGAAAGAGCGCTTACGCA 1562
Qy 1886 TCCTGAGCTTACTGATGATGATGTCACAGATCTTAATGGCTGTGATCCACCAAC 1945
Db 1563 CAAGGACCGCGCTCTGTCATGTGACGACCAACCCGAGGCTGTCTCATCGCGGAA 1622
Qy 1946 CATCAGTGGGAACAGTCTATGGATTCAGCAAGCGCGCCAGCAACCGCTTGTGGTGG 2005
Db 1623 GATCAGCGCGGAGATGTGACGCGCTTGGCGCTGTCCGGTGTGAAGATGTCTGTGACGG 1682
Qy 2006 AGGAGTAGAGGATGATGATCTGCGCGCTTGCACATTAAGGAATATTTCTACTTC 2062
Db 1683 CGGGTGGCGCGGATGTGACAGATGCGCGCTCTCAACCTGCGGAACGTCCCGCTCC 1739

RESULT 14
US-09-815-242-9898
Sequence 9898, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Cair, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA 0114
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 1410
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9898
LENGTH: 1719
TYPE: DNA
ORGANISM: Salmonella typhi
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1719)
US-09-815-242-9898

Query Match 16.0%; Score 344.8; DB 9; Length 1719;
Best Local Similarity 52.5%; Pred. No. 2,1e-102;
Matches 904; Conservative 0; Mismatches 797; Indels 21; Gaps 6;

327 ATGCACACAGCTACGACGAGAACATTTATTGACACTTTGGAGCTCAAGGTGACCGA 386
1 ATGAACAAACCGTTGTCTTTATTCGCAAAACCGTGGACAGCGCTGGCGTAAAACAA 60
387 ATTATGTTTGGTGGTGAACAGCTTAA--TCCGATCGGATGCTGTCCGCATCA 443
61 ATCTGGGGGCTCACTGGCGACTCCCTTAACGGCCTGAGCCATAGCTTTAAATCGATGGA 120
444 GATATTGATGGTGCACGTTTGAATAGAGAAAGCGCGGCTTTGACGCGGTGCGAA 503
121 ACCATTGAATGATGCAACCCCGCACGAGAGAGTGCCTTTCGCGCGCGCGCA 180
504 TCGTTGATCCTGGGAGCTGGAGATATGCTGCTCTTCTGTGCTCTGAAACACAC 563
181 GCGACCTTACCGGACGTCGAGTGTGCGCGGTATTCAGTGAACCGGCAACCTCCAC 240
564 CTGATTCAGGCTCTTATGATTCGATCGCAATGATGTCGAAAGTGTGGCCATCGCTAC 623
241 CTGATCAATGGCTGTTGATTTGCCACCGTAACCGATCCCTGTTCTGGGATGCGCC 300
624 CATATTCGAGTCCAGATGTTGACGTTTCCAGAGAAACGATCCGAGATTTG 683
301 CATATTCGCTCCAGTAAATCGGACGCTTATTCAGAGAACCCGACCGGAGGTG 360
684 TTTAAGGAATGCTCTGTTACTGCGAGATGATGATGATGATGATGATGATGATGAT 743
361 TTCCGTAATGCAACCGCACTATTCGATGTTTCCAGCCCGGAGATCCGCGAGTA 420
744 TTGCATCAGCGATTCAGTCCACCATGCGGGTAAAGTGTGCGGTGATGATTTCT 803
421 CTGCGCATCGCATGCGCAAGAGGTGTAATCGCGCGCTCTCCGTGCTGCTACTTCC 480
804 GGTGATATGCTAAGAGACGAGTGAAGCTTATTCATTCATTCATTCATTCATTCAT 863
481 GGTGATGCTGCTGAAACCGCGCTGAAACCGCGTCAACCATTCATTCATTCATTCAT 923
864 GGCATCTCTGCTGTTCCCGGATCTTACTGAGGCTGCAAGCGTGTGATGAGGATTAAC 983
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658 GTGCGGTTGGCGCAAACTAAAGCGCAATCGTTCATGCTGCGCGCAAGAGAC 717
1044 ATCCAGCATGAGATCCGTTTGAAGTGGCATGCTGCGCTGCTGCTGCTGCTGCTGCT 1103
718 GTTGAATGATTAACCTTATGATGAGGATGACCGGCTGATTTGCTTCTTCTGCG 777
1104 GTGAGTGGCTCCATGAGCGGATGCTGCTGATTTGATGATGATGATGATGATGATGAT 1163
778 TTCCACACCATGATGACGCCCATGCTGATGCTGCTGCGACCCAGTTCCCTATGCG 837
1164 GATTTCTTCTCTA---AAGACAAGCTTGGCCAGGATGATGATGATGATGATGATGAT 1220
838 GCTTTTATTCGAGGATGCAAAATCATTCAGATGATGATGATGATGATGATGATGATGAT 897
1221 CGAGCTACACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1280
898 GCGCAGAGAAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
1281 TTGCTCATGATGAGAGAAAAACAGATGCTTCTTCTGATGATGATGATGATGATGATGAT 1340
958 CTGCGCTGATGAGAGAAAAACAGATGCTTCTTCTGATGATGATGATGATGATGATGAT 1014
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1015 TATCGGAGCGCCCGTAAGGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1400
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1401 ATTACCTGATATGCTTGCCTTATTTTGAACGAGCTGGCGATTAAGATGCGTCTTT 1460
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1821 ATCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1880
1486 ATTCAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1545
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1546 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1605
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RESULT 15
US-09-965-825-12
; Sequence 12, Application US/09965825
; Patent No. US2002015099A1
; GENERAL INFORMATION:
; APPLICANT: DUSCH, Nicole
; APPLICANT: THOMAS, Herman
; APPLICANT: THIERBACH, Georg
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENIC ACID
; TITLE OF INVENTION: CORYNEFORM BACTERIA
; FILE REFERENCE: 21354USX
; CURRENT APPLICATION NUMBER: US/09/965,825
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: DE 10048604.5
; PRIOR FILING DATE: 2000-09-30
; PRIOR APPLICATION NUMBER: DE 10117085.8
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1422
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-965-825-12
Query Match 15.0%; Score 324.4; DB 10; Length 1422;
Best Local Similarity 99.7%; Pred. No. 1e-95;
Matches 325; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 398 TTAGAGCGATTCTGTGAGGTCACTTTTGTGGGTCGGGGTCTAAATTGGCCAGTTT 457
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OY 61 CGAGCGACACAGACAGGCGTGCCACGATGTTAAATAGCGCGATCGGTGCGCATCTGTGT 120
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Db 458 CGAGCGACACAGACAGGCGTGCCACGATGTTAAATAGCGCGATCGGTGCGCATCTGTGT 517
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OY 241 AAGCGTGGCAACACTGGAATTTAAGACACATGTAAGTGCACCAAGTTAGGCAACAC 300
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Db 638 AAGCGTGGCAACACTGGAATTTAAGACACATGTAAGTGCACCAAGTTAGGCAACAC 697
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OY 301 AATAGCCATAACGTTGAGAGTTCAG 326
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Db 698 AATAGCCATAAAGTTGAGAGTTCAG 723
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